

445

```

      245      250      255
Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu
      260      265      270
Met Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr
      275      280      285
Ala Val Tyr Leu Ala Ile Gly Val Ala Val Leu Leu Ile Ser Leu Ala
      290      295      300
Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg
305      310      315

```

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537

```

Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser
1      5      10      15
Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe
      20      25      30
Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp
      35      40      45
Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser
      50      55      60
Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe
      65      70      75      80
Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu
      85      90      95
Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile
      100      105      110
Gly Gly Leu Ser Phe Leu
      115

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

446

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

```

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1      5      10      15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
20      25      30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
35      40      45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
50      55      60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65      70      75      80
Phe Ile Phe Ser His Phe Phe Ser
85

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

```

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val
1      5      10      15
Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe
20      25      30
Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala
35      40      45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
50      55      60
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65      70      75      80
Phe Ile Phe Ser His Phe Phe Ser
85

```

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

447

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539

```

Met Phe Lys Ser Arg Leu Asn Ser Trp Ile Leu Leu Gly Ile Leu Gly
 1           5           10           15
Val Leu Val Val Val Phe Trp Asp Val Ile Lys Tyr Lys Ile Glu Asp
          20           25           30
Leu Gln His Asp His Tyr Leu Ser Gln Val Lys Glu Arg Glu Glu Tyr
          35           40           45
Tyr Lys Asn His Ile Glu Glu Ala Leu Lys Lys Asp Ser Glu Cys Phe
          50           55           60
Glu Lys Gly Gly Asp Lys Val Asp Cys Ser Ala Ala Met Arg Ile Ala
65           70           75           80
Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys
          85           90

```

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540

```

Met Val Phe Trp Gly Ala Val Phe Phe Leu Trp Asp Arg Thr Ala Trp
 1           5           10           15
Lys Arg Leu Met Val Phe Leu Asn Ser Leu Unk Unk Met Leu Ala Ala
          20           25           30
Leu Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His
          35           40           45
Thr Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met
          50           55           60
Gly Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe
65           70           75           80
Val Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu
          85           90           95
Asn Gln Met His Ala Glu Phe Ile Asp Val Ser Ile His Phe Tyr Ala
          100          105          110
Leu Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu
          115          120          125
Ser Ser Leu Lys Lys Ala Cys Glu Asn Ala
          130          135

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids

SUBSTITUTE SHEET (RULE 26)

448

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

```

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1      5      10      15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
20      25      30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
35      40      45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
50      55      60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65      70      75      80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
85      90      95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
100     105     110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
115     120     125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
130     135     140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145     150     155     160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
165     170     175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
180     185     190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
195     200     205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
210     215     220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225     230     235     240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245     250     255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
260     265     270
Lys Lys Ser Pro
275

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

449

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

```

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1      5      10      15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
20     25     30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
35     40     45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
50     55     60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65     70     75     80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
85     90     95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
100    105    110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
115    120    125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
130    135    140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145    150    155    160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
165    170    175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
180    185    190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
195    200    205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
210    215    220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225    230    235    240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245    250    255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
260    265    270
Lys Lys Ser Pro
275

```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...254

SUBSTITUTE SHEET (RULE 26)

450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542

```

Met His Glu Gln Gly Ser Ile Ser Phe Ile Gly Glu Gln Gly Ala Lys
1      5      10      15
Arg Leu Leu Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn
20      25      30
Lys Ile Ala Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val
35      40      45
Ala Arg Thr Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe
50      55      60
Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys
65      70      75      80
Asp Tyr Arg Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr
85      90      95
Val Met Tyr Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg
100     105     110
Tyr Gly Phe Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys
115     120     125
Glu Ser Leu Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu
130     135     140
Lys Thr Leu Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn
145     150     155     160
Lys Cys Ile Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu
165     170     175
Val Leu Asn Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr
180     185     190
Ser Ile Leu Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile
195     200     205
Lys Lys Ser Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp
210     215     220
Tyr Arg Leu Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys
225     230     235     240
Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro
245     250

```

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

```

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1      5      10      15
Arg Ala Thr His Leu Tyr Leu Gly Glu Pro Lys Tyr Lys Asp Asn
20      25      30
Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
35      40      45
Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
50      55      60
Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu

```

SUBSTITUTE SHEET (RULE 26)

451

```

65          70          75          80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
      85          90          95
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
      100         105         110
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
      115         120         125
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
      130         135         140
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
      145         150         155         160
His Val Lys Phe Ile Tyr Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
      165         170         175
Ile Leu Gly Gln Leu Gln Ile Phe Ser
      180         185

```

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

```

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
1          5          10          15
Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
      20          25          30
Phe Glu Lys Gly Met
      35

```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

452

```

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1          5          10          15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
          20          25          30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
          35          40          45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
          50          55          60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65          70          75          80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
          85          90

```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

```

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1          5          10          15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
          20          25          30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
          35          40          45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
          50          55          60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys
65          70          75          80
Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg
          85          90

```

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

SUBSTITUTE SHEET (RULE 26)

453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

```

Val Gly Lys Ser Leu Arg Tyr Ser Leu Asn Leu Asp Leu Asn Gln Lys
1      5      10      15
Ala Asp Leu Phe Phe Thr Glu Leu Glu Pro Thr Gly Leu Thr Leu Ser
      20      25      30
Pro Ile Met Lys Arg Phe Thr Ile Lys Gly Asp Phe Asp Ser Gly Leu
      35      40      45
Lys Ser Tyr Asp Met Ser Tyr Met Tyr Ala Ser Leu Gln Ala Ile Ser
      50      55      60
Ala Ile Arg Arg Leu Pro Leu Gly Leu Tyr Asp Gly Val His Val Tyr
      65      70      75      80
Ser Lys Thr Pro Met Lys Asp Ile Glu Lys Leu Arg Asn Ala Leu Lys
      85      90      95
Thr Ile Asn His His Gly Ile Gly Ile Glu Gly Trp Trp Gln Gln Asn
      100      105      110
Gly Asn Phe Phe Ser Ala Met Glu Leu Glu Lys Arg Ala Leu Phe Ile
      115      120      125
Val Leu Met Leu Ile Ile Leu Met Ala Ser Leu Asn Ile Ile Ser Ser
      130      135      140
Leu Leu Met Val Val Met Asn Arg Arg Lys Glu Ile Ala Leu Leu Phe
      145      150      155      160
Ser Met Gly Ser Ser Gln Lys Glu Ile Gln Lys Thr Phe Phe Tyr Leu
      165      170      175
Gly Asn Ile Ile Ser Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

```

Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Ile
1      5      10      15
Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro
      20      25      30
His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly
      35      40      45
Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp
      50      55      60
Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val
      65      70      75      80
Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu Pro Thr Asn His
      85      90      95
Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His
      100      105      110
Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala
      115      120      125

```

SUBSTITUTE SHEET (RULE 26)

454

```

His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu Val Leu Ala Ile
 130          135          140
Gly Phe Glu Glu Gly Lys Glu Asn Pro Asn Leu Asp Pro Ile Leu Glu
145          150          155          160
Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala Phe
          165          170          175
Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr Ala
          180          185          190
Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro Leu
          195          200          205
Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys Asn
210          215          220
Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile Ile
225          230          235          240
Lys Ser Ser Ala Glu Thr Arg
          245

```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

```

Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr Leu Ala Leu Gly
 1          5          10          15
Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe Phe Asp Asp Lys
          20          25          30
Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu Cys Tyr Pro Ser
          35          40          45
Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile Val Ser Pro Gly
50          55          60
Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys His Leu Met Ser
65          70          75          80
Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser Phe Thr Pro Thr
          85          90          95
Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr Thr Thr Glu Met
          100          105          110
Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser Gly Gly Asn Ile
          115          120          125
Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser Pro Leu Trp Val
130          135          140
Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn Lys Ala Tyr Pro
145          150          155          160
Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His Leu Thr Trp His
          165          170          175
Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys Val Leu Thr Leu
          180          185          190
Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys Phe Lys Glu His
          195          200          205
Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe Phe Asp Lys Ser

```

SUBSTITUTE SHEET (RULE 26)

455

```

      210              215              220
Glu Glu Val Leu Glu Cys Leu Lys Ile Pro Ser Asn Ala Leu Phe Phe
225              230              235              240
Lys Gly Ala Phe Leu Leu Asp Ala Ala Leu Ala Leu Leu Val Tyr Glu
      245              250              255
Gln Phe Leu Lys Ile Lys Asn Leu Lys Trp Gln Asp Tyr Arg Glu Asn
      260              265              270
Ala Leu Lys Arg Leu Asn Ala Phe Lys Ile Gly Ser His Lys Met Glu
      275              280              285
Glu Phe Arg Asp Lys Gln Gly Arg Leu Trp Val Asp Asp Ser Lys Ala
      290              295              300
Thr Asn Ile Asp Ala Thr Leu Gln Ala Leu Lys Thr Phe Lys Asn Gln
305              310              315              320
Lys Ile His Leu Ile Leu Gly Gly Asp Ile Lys Gly Val Asn Leu Thr
      325              330              335
Pro Leu Phe Glu Glu Phe Lys Asn Tyr Lys Ile Ser Leu Tyr Ala Ile
      340              345              350
Gly Ser Ser Ala Ser Ile Ile Gln Ala Leu Ala Leu Glu Phe Asn Val
      355              360              365
Ser Cys Gln Val Cys Leu Lys Leu Glu Lys Ala Val Gln Glu Ile Lys
      370              375              380
Ser Val Leu Leu Gln Asn Glu Val Ala Leu Leu Ser Pro Ser Ala Ala
385              390              395              400
Ser Leu Asp Gln Phe Ser Ser Tyr Lys Glu Arg Gly Glu Lys Phe Lys
      405              410              415
Ala Phe Val Leu Lys Asp
      420

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

```

Met Ala His His Unk Glu Gln His Gly Gly His His His His His His
1              5              10              15
His Thr His His His His Tyr His Gly Gly Glu His His His His His
      20              25              30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
      35              40              45
His Gln Glu Glu Gly Cys Cys His Gly Unk His Glu
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

456

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

```

Met Ala His His Unk Glu Gln His Gly Gly His His His His His His
1      5      10      15
His Thr His His His Tyr His Gly Gly Glu His His His His His His
20     25     30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
35     40     45
His Gln Glu Glu Gly Cys Cys His Gly Unk His Glu
50     55     60

```

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550

```

Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1      5      10      15
Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn
20     25     30
Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys
35     40     45
Asp His Gln Ile Asn Ser
50

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

457

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1      5      10      15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
20      25      30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
35      40      45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
50      55      60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65      70      75      80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
85      90      95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
100     105     110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
115     120     125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
130     135     140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145     150     155     160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
165     170     175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
180     185     190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
195     200     205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
210     215     220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225     230     235     240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
245     250     255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
260     265     270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
275     280     285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
290     295

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

458

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1      5      10      15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
      20      25      30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
      35      40      45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
      50      55      60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65      70      75      80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
      85      90      95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
      100     105     110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
      115     120     125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
130     135     140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145     150     155     160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
      165     170     175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
      180     185     190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
      195     200     205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
210     215     220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225     230     235     240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
      245     250     255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
      260     265     270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
      275     280     285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
290      295

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser

SUBSTITUTE SHEET (RULE 26)

459

```

1           5           10           15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ile Val Leu Leu Ile Ser
      20           25           30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
      35           40           45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
      50           55           60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
65           70           75           80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
      85           90

```

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

```

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1           5           10           15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ile Val Leu Leu Ile Ser
      20           25           30
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
      35           40           45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
      50           55           60
Ile Thr Phe Phe Ala Ala Unk Arg Leu Gly Unk Ser Arg Leu Ser Tyr
65           70           75           80
Asp His Glu Leu Leu Val Phe Phe Leu Unk
      85           90

```

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

SUBSTITUTE SHEET (RULE 26)

460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553

```

Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn Arg Ala Arg
1      5      10      15
Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val Thr Trp Trp
      20      25      30
Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser Leu Val Ser
      35      40      45
Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe Ser Leu Ser
      50      55      60
Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg Ser Leu Ala
      65      70      75      80
Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe Ser Val Phe
      85      90      95
Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Leu Phe Cys His Asn
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

```

Met Gln Lys Met Gly Val Val Ser Tyr Ser Val Phe Gln Ala Phe Glu
1      5      10      15
Lys Ala Leu Ser Arg Phe Lys Glu Gly Val Val Leu Ile Val Asp Ser
      20      25      30
Leu Arg Arg Leu Ile Met Gly Ser Ala Ser Val Lys Glu Leu Ser Gly
      35      40      45
Val Ile Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser Val Ser Met
      50      55      60
Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly Ile Leu Asn
      65      70      75      80
Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu Gly Val Val
      85      90      95
Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro Ile Gln Asn Ala
      100      105      110
Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val Met Phe Leu Gly
      115      120      125
Leu Phe Asn Asp Ile Thr Arg Leu Leu
      130      135

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

461

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555

```

Val Met Ala Leu Leu Lys Ile Ser Val Val Val Pro Glu Gly Glu Val
1      5      10      15
Tyr Thr Gly Glu Val Lys Ser Val Val Leu Pro Gly Val Glu Gly Glu
20     25     30
Phe Gly Val Leu Tyr Gly His Ser Asn Met Ile Thr Leu Leu Gln Ala
35     40     45
Gly Val Val Glu Ile Glu Thr Glu Asn Gln Lys Glu His Ile Ala Ile
50     55     60
Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu Arg Val Asp Ile Leu Ala
65     70     75     80
Asp Gly Ala Val Phe Ile Lys Lys Gly Ser Asp Asp Arg Asp Asp Ala
85     90     95
Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp Ala Ser Ser Asp Arg Leu
100    105    110
Ala Val Ser Ser Val Leu Ala Lys Ile Glu Ser Leu
115    120

```

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556

```

Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1      5      10      15
Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
20     25     30
Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
35     40     45
Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
50     55     60
Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65     70     75     80
Ile Ser Gln Ala Ile Ile
85

```

SUBSTITUTE SHEET (RULE 26)

462

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1          5          10          15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
          20          25          30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
          35          40          45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
          50          55          60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65          70          75          80
Pro Met Lys Ile Gln Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1          5          10          15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
          20          25          30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
          35          40          45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
          50          55          60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65          70          75          80
Pro Met Lys Ile Gln Lys

```


(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558

```

Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1      5      10      15
Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
20      25      30
Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
35      40      45
Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
50      55      60
Gln Lys Val Thr Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65      70      75      80
Lys Phe Asp Asp Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
85      90      95
Gly Ile Asn Ala Met Trp Gly Ile Gln Asn Leu Leu
100      105

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

```

Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
1      5      10      15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
20      25      30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
35      40      45

```

464

```

Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
 50          55          60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
 65          70          75          80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
          85          90          95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
          100          105          110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
          115          120          125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
 130          135          140

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

```

Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
 1          5          10          15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
          20          25          30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
          35          40          45
Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
 50          55          60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
 65          70          75          80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
          85          90          95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
          100          105          110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
          115          120          125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
 130          135          140

```

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

465

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

```

Met Ile Asp Asn Leu Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys
1      5      10      15
Ala Tyr Ala Phe Leu Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala
20      25      30
Leu Arg Met Thr His Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile
35      40      45
Gly Asn Leu Gly Phe Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp
50      55      60
Phe Leu Gln Asp Leu Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu
65      70      75      80
Ala Leu Glu Gly Arg Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu
85      90      95
Ile Val Ile Ala Lys Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala
100     105     110
Cys Ala Gly His Thr Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile
115     120     125
Ile Ala Thr Pro Leu Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly
130     135     140
Pro Ile Val His Ala Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys
145     150     155     160
Asp Phe Ser Leu Thr Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys
165     170     175
Leu Ser Phe Cys Ala His Glu Asp Ala Leu Val Val Ile Asp Gly Gln
180     185     190
Ala Thr Tyr Asp Leu Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser
195     200     205
Pro Thr Thr Lys Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys
210     215     220
Val Leu Lys Glu Lys Leu Leu
225     230

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1      5      10      15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
20      25      30

```

SUBSTITUTE SHEET (RULE 26)

466

```

Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
 35      40      45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
 50      55      60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
 65      70      75      80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
      85      90      95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
      100      105      110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
      115      120      125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
      130      135      140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
      145      150      155      160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
      165      170      175
Cys Lys Lys Lys Asn Thr Ser Ser Arg
      180      185

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
 1      5      10      15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
      20      25      30
Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
      35      40      45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
      50      55      60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
      65      70      75      80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
      85      90      95
Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
      100      105      110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
      115      120      125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
      130      135      140
Ser Glu Ser Tyr Unk Tyr Gly Leu Gly Val Glu Lys Unk Unk Lys Lys
      145      150      155      160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
      165      170      175
Cys Lys Lys Lys Asn Thr Ser Ser Arg

```

SUBSTITUTE SHEET (RULE 26)

467

180

185

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562

```

Met Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu
1           5           10           15
Ala His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met
          20           25           30
Arg Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile
          35           40           45
Leu Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu
          50           55           60
Glu Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val
          65           70           75           80
Gly Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu
          85           90           95
Phe Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val
          100          105          110
Pro Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile
          115          120          125
Gly Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe
          130          135          140
Leu Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val
          145          150          155          160
Leu Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu
          165          170          175
Ala Leu Gln Gln Leu Arg Ser
          180

```

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

468

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563

```

Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn Asn Leu
1      5      10      15
Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala Ile Ala
      20      25      30
Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro Leu Lys
      35      40      45
Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu Asp Ala
      50      55      60
Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala Ser Phe
      65      70      75      80
Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys Lys Gln
      85      90      95
Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly Val Ser
      100     105     110
Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile Pro Leu
      115     120     125
Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe Val Ala
      130     135     140
Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
145      150

```

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564

```

Val Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser
1      5      10      15
Phe Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser
      20      25      30
Lys Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr
      35      40      45
Ile Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala
      50      55      60
Phe Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn
      65      70      75      80
Ser Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu
      85      90      95
Leu Ser Tyr Pro Asn Asp Pro Asn Asn Asn Glu Asp Asn Ala Asn Asn
      100     105     110
Ser Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn
      115     120     125
Pro Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn
      130     135     140
Gly Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile

```

SUBSTITUTE SHEET (RULE 26)

469

```

145          150          155          160
Gln Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp
          165          170          175
Arg Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala
          180          185          190
Gln Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly
          195          200          205
Ser Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys
          210          215          220
Ser Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu
          225          230          235          240
Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu
          245          250          255
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu
          260          265          270
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
          275          280          285

```

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565

```

Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser Asn Pro Leu Val
1          5          10          15
Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr Leu Tyr Pro Asn
          20          25          30
Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu Tyr Ser Glu Ile
          35          40          45
Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu Lys Gly Ile Gly
          50          55          60
Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met Val Leu Gly Met
          65          70          75          80
Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln Asn Asn Asp Leu
          85          90          95
Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe Val Gly Tyr Leu
          100          105          110
Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser Ser Ser Gly Asn
          115          120          125
Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr Glu Ile Phe Asp
          130          135          140
Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn Val Val Lys Glu
          145          150          155          160
Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile Asp Thr His His
          165          170          175
Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg Gln Ile Leu Thr
          180          185          190
Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn Asn Gly Leu Ser
          195          200          205

```

SUBSTITUTE SHEET (RULE 26)

470

```

Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val Ile Leu Gly Leu
210                215                220
Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val Phe Met Thr Tyr
225                230                235                240
Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe Met Leu Leu Leu
                245                250                255
Gly Phe Phe Gln Thr Arg Gly Phe Leu Val Ser Tyr Val Lys Lys
                260                265                270
Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu Leu Val Leu
275                280                285
Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val Gly Gly Ser Asn
290                295                300
Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile Gly Ile Ser Leu
305                310                315                320
Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala Ile Phe Gly Thr
                325                330                335
Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr Gln Gly Val Gln
                340                345                350
Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser Leu Lys Ser Val
355                360                365
Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr Lys Asp Ala Lys
370                375                380
Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp Met Pro Gly His
385                390                395                400
Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu Pro Lys Ser His
                405                410                415
Arg Ala Ser Lys
                420

```

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566

```

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
1          5          10          15
Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
20          25          30
Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
35          40          45
Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
50          55          60
Gln Val Asn Tyr Lys Ser Ala Pro
65          70

```

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

471

(A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

```

Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly
1      5      10      15
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly
20      25      30
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu
35      40      45
Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser
50      55      60
Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro
65      70      75      80
Lys Lys Arg Trp Lys Tyr Ala Gly Ile Met Leu Ile Ser Gly Pro Leu
85      90      95
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu
100     105     110
Val Ser Ile Ser Phe Asn Leu Pro Ser Ser Ile Gln Glu Ser Glu Gln
115     120     125
Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu
130     135     140
Phe Ser Val Leu Phe Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys
145     150     155     160
Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala
165     170     175
Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser
180     185     190
Lys Ala Phe His Phe Met Leu Ile Ser Ser Gln Lys Ile
195     200     205

```

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568

SUBSTITUTE SHEET (RULE 26)

472

```

Met Glu Lys Val Cys Val Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu
1      5      10      15
Glu Arg Leu Lys Glu Lys Tyr Gly Asp Trp Glu Lys His Val Lys
20     25     30
Ala Lys Ala Ile Asn Glu Glu Leu Glu Glu Gln Val Lys Ala Lys
35     40     45
Ala Lys Glu Gln Gln Lys Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe
50     55     60
Leu Lys Lys Val Gly Leu Lys Lys Arg Asp Met Leu Gln Ser Thr Met
65     70     75     80
Leu Phe Asp Glu Val Lys Glu Ala Asp Val Leu Phe Gln Ala Glu Arg
85     90     95
Lys Ile Gly Asp Trp Ile Phe Ser Ser Ala Val Phe Phe Phe Ala Leu
100    105    110
Ala Leu Ile Glu Ala Ile Ile Ile Val Cys Leu Leu Pro Leu Lys Glu
115    120    125
Lys Val Pro Tyr Leu Val Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala
130    135    140
Ile Val Gln Arg Ala Asp Lys Ser Ile Arg Ala Asn Gln Ala Leu Val
145    150    155    160
Arg Gln Leu Val Ala Ser Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser
165    170    175
Ile Lys Glu Gln Asn Glu Ile Ala His Glu Thr Ile Arg Leu Gln Ser
180    185    190
Ala Phe Glu Val Trp Asp Phe Phe Glu Lys Leu Val Ser Tyr Glu His
195    200    205
Ser Ile Tyr Thr Asn Ile Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn
210    215    220
Ile Ala Leu Ile Ser Lys Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln
225    230    235    240
Leu Phe His Lys Glu Lys Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile
245    250    255
Met Thr Phe Glu Phe Glu Pro Ile Glu Ile Asp Thr Lys Ser Val Pro
260    265    270
Leu Asn Pro Thr Gly Phe Ile Val Thr Gly Tyr Asp Val Thr Glu Ile
275    280    285
Ala Ile Leu Lys Asp Leu Asp Glu Lys Asn Lys Val Lys Asp Asp Gly
290    295    300
Val Lys Ser Arg Ile Ile His Val Glu Lys Lys Asp Pro His Met Ser
305    310    315    320
Gln Tyr Lys Asp Val Lys Glu Gln
325

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn

SUBSTITUTE SHEET (RULE 26)

473

```

1           5           10           15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
      20      25      30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
      35      40      45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
      50      55      60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
      65      70      75      80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
      85      90      95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
      100      105      110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
      115      120      125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
      130      135

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

```

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
1           5           10           15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
      20      25      30
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
      35      40      45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
      50      55      60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
      65      70      75      80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
      85      90      95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
      100      105      110
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu
      115      120      125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
      130      135

```

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

474

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...76
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570

```

Met Leu His Lys Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly
1           5           10           15
Ile Phe Cys Val Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met
20           25           30
Val Ala Phe Lys Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly
35           40           45
Ser Val Val Phe Leu Trp Ser Asp Leu Leu Val Phe Val Gly Phe Lys
50           55           60
Asn Ile Ser Phe Val Leu Asp Ile Gly Tyr Glu Ile
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1           5           10           15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
20           25           30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
35           40           45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
50           55           60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65           70           75           80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
85           90           95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
100          105          110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
115          120          125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
130          135          140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu

```

SUBSTITUTE SHEET (RULE 26)

475

```

145          150          155          160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
          165          170          175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
          180          185          190
Phe

```

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1      5      10      15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
      20      25      30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
      35      40      45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
      50      55      60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
      65      70      75      80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
      85      90      95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
      100      105      110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
      115      120      125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
      130      135      140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
      145      150      155      160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
      165      170      175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
      180      185      190
Phe

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

476

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

```

Met Pro Phe Leu Lys Asn Trp Ile Trp Ser Leu Lys Met Ala Leu Ser
1           5           10           15
Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
          20           25           30
Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
          35           40           45
Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
          50           55           60
Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
65           70           75           80
Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
          85           90           95
Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
          100          105          110
Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
          115          120          125
Tyr Ile Gln Asn Lys Asn Lys Arg Leu Ala Pro Phe
130           135           140

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

```

Met Pro Gln Asn Gln Leu Val Ile Thr Ile Ile Asp Glu Ser Gly Ser
1           5           10           15
Lys Gln Leu Lys Phe Ser Lys Asn Leu Lys Arg Asn Leu Ile Ile Ser
          20           25           30
Val Val Ile Leu Leu Leu Ile Val Gly Leu Gly Val Gly Phe Leu Lys
          35           40           45
Phe Leu Ile Ala Lys Met Asp Thr Met Thr Ser Glu Arg Asn Ala Val
          50           55           60
Leu Arg Asp Phe Arg Gly Leu Tyr Gln Lys Asn Tyr Ala Leu Ala Lys
65           70           75           80
Glu Ile Lys Asn Lys Arg Glu Glu Leu Phe Ile Val Gly Gln Lys Ile
          85           90           95
Arg Gly Leu Glu Ser Leu Ile Glu Ile Lys Lys Gly Ala Asn Gly Gly

```

SUBSTITUTE SHEET (RULE 26)

477

```

      100      105      110
Gly His Leu Tyr Asp Glu Val Asp Leu Glu Asn Leu Ser Leu Asn Gln
      115      120      125
Lys His Leu Ala Leu Met Leu Ile Pro Asn Gly Met Pro Leu Lys Thr
      130      135      140
Tyr Ser Ala Ile Lys Pro Thr Lys Glu Arg Asn His Pro Ile Lys Lys
      145      150      155      160
Ile Lys Gly Val Glu Ser Gly Ile Asp Phe Ile Ala Pro Leu Asn Thr
      165      170      175
Pro Val Tyr Ala Ser Ala Asp Gly Ile Val Asp Phe Val Lys Thr Arg
      180      185      190
Ser Asn Ala Gly Tyr Gly Asn Leu Val Arg Ile Glu His Ala Phe Gly
      195      200      205
Phe Ser Ser Ile Tyr Thr His Leu Asp His Val Asn Val Gln Pro Lys
      210      215      220
Ser Phe Ile Gln Lys Gly Gln Leu Ile Gly Tyr Ser Gly Lys Ser Gly
      225      230      235      240
Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe Leu Gly Lys
      245      250      255
Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp His Phe Gln
      260      265      270
Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn Leu Phe Trp
      275      280      285
Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp Lys Asp Thr
      290      295      300
Leu Lys Gly Gln
305

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574

```

Met Ile Thr Gly Ser His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile
1      5      10      15
Thr Leu Asn Gln Asn Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys
      20      25      30
Asn Thr Leu Leu Asn Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr
      35      40      45
Pro Glu Lys Val Asn Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys
      50      55      60
Asp Phe Lys His Leu Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe
      65      70      75      80
Gly Asn Gly Val Gly Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu
      85      90      95
Asn Ile Asp Phe Ser Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro
      100      105      110
Asn His His Pro Asp Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu
      115      120      125

```

SUBSTITUTE SHEET (RULE 26)

478

```

Lys His Met Arg Glu Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly
130          135          140
Asp Ala Asp Arg Ile Ala Met Leu Ser Ser His His Ile Tyr Ala Gly
145          150          155          160
Asp Glu Leu Ala Ile Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile
          165          170          175
Thr Pro Phe Val Ile Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn
          180          185          190
Ala Ile Asn Thr Phe Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser
          195          200          205
Asn Leu Lys Ile Lys Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu
210          215          220
Met Ser Gly His Ile Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp
225          230          235          240
Ala Leu Tyr Ala Cys Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser
          245          250          255
Pro Ser Asp Leu Glu Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr
          260          265          270
Thr Pro Glu Glu Lys Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile
275          280          285
Ile Arg Asn Leu Gln Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro
290          295          300
Thr Ile Lys Glu Ile Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu
305          310          315          320
His Gly Phe Gly Leu Ile Arg Ala Ser Asn Thr His Pro Leu Phe Ser
          325          330          335
Gln Pro Leu

```

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575

```

Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Unk Pro Gln
1          5          10          15
Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala Phe
          20          25          30
Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile Thr
          35          40          45
Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met Val
          50          55          60
Phe Ile Ser Ala Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly Val
          65          70          75          80
Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala Phe
          85          90          95
Gly Met Met Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys Gln
          100          105          110
Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu Leu

```

SUBSTITUTE SHEET (RULE 26)

479

```

      115              120              125
Thr Leu Ile Leu Ser Ala Pro Ser Ile Unk Glu Asn Leu Ser Lys Gln
  130              135              140
Val Asn Ser Asn Ala Ile Asp Ala Gln Unk Pro Asn Ile Lys Ala Ile
  145              150              155              160
Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala Ala
      165              170              175
Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile Gln
      180              185              190
Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu
      195              200              205

```

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576

```

Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu
 1              5              10              15
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met
 20              25              30
Leu Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe
 35              40              45
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser
 50              55              60
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn
 65              70              75              80
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr
      85              90              95
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
      100              105              110
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
      115              120              125
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
      130              135              140
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
 145              150              155              160
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
      165              170              175
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
      180              185              190
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
      195              200              205
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
 210              215              220
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
 225              230              235              240
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
      245              250

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577

```

Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu
1           5           10           15
Ser Gln Val Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro
20           25           30
Phe Ala Gly Ile Val Ala Gly Ala Met Thr Ala Ala Ile Ile Pro Ile
35           40           45
Val Val Gly Phe Thr Asn Pro Gln Met Thr Asp Ile Ile Asn Pro Ile
50           55           60
Lys Ser Lys His Arg
65

```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

```

Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys
1           5           10           15
Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val
20           25           30
Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu
35           40           45
Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu
50           55           60
Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys
65           70           75           80
Lys Leu Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser

```

481

	85		90		95
Val Gly Val	Asn Ala Met Ile Leu Ser	Leu Leu Tyr Lys Lys	Pro Pro		
	100	105	110		

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579

```

Met Asp Glu Unk Leu Val Tyr Gly Val Ile Cys Met Pro Ser Gln Val
1      5      10      15
Phe Ala Asn Thr Gly Thr Asn Val Ser Ile Ile Phe Phe Gln Lys Thr
20     25     30
Pro Ser Ala Lys Glu Val Ile Leu Ile Asp Ala Ser Lys Leu Gly Glu
35     40     45
Glu Tyr Thr Glu Asn Lys Asn Lys Lys Thr Arg Leu Arg Pro Ser Asp
50     55     60
Met Asp Leu Ile Leu Glu Thr Phe Gln Asn Lys Ala Pro Lys Ser Asp
65     70     75     80
Phe Cys Ala Leu Val Ser Phe Asp Glu Ile Thr Glu Lys Asn Tyr Ser
85     90     95
Leu Asn Pro Gly Gln Tyr Phe Thr Ile Glu Asp Thr Ser Glu Thr Ile
100    105    110
Ser Gln Ala Glu Phe Glu Asn Leu Met Gln Gln Tyr Ser Ser Glu Leu
115    120    125
Ala Ser Leu Phe Asp Glu Ser Gln Asn Leu Gln Gln Glu Ile Leu Glu
130    135    140
Thr Leu Lys Gly Val Arg Phe Glu
145    150

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

SUBSTITUTE SHEET (RULE 26)

482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

```

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1           5           10           15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
          20           25           30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
          35           40           45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
          50           55           60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65           70           75           80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
          85           90           95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
          100          105          110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
          115          120          125
Pro

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

```

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1           5           10           15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
          20           25           30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
          35           40           45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
          50           55           60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65           70           75           80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
          85           90           95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
          100          105          110
Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
          115          120          125
Pro

```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

483

(A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

```

Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg Leu Gly Tyr Glu Asp
1          5          10          15
Val Leu Glu Ala Glu His Gly Val Glu Ala Trp Glu Lys Leu Asp Ala
20          25          30
Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp Asn Met Pro Glu Met
35          40          45
Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala Asp Asn Arg Phe Lys
50          55          60
Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly Gly Lys Ala Glu Val
65          70          75          80
Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr Ile Val Lys Pro Phe
85          90          95
Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val Val Leu Gly Thr Asn
100          105          110
Asp

```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

```

Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser
1          5          10          15
Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu
20          25          30
Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser
35          40          45
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met
50          55          60
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

484

```

Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn
      85                      90                      95
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu
      100                      105                      110
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr
      115                      120                      125
Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu
      130                      135                      140
Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys
      145                      150                      155                      160
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn
      165                      170

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

```

Met Gly Cys Phe Ser Thr Ile Cys Cys Lys Gly Leu Thr Leu Ser Val
1      5                      10                      15
Gly Gly Phe Leu Val Met Met Arg Phe Leu Ile Phe Lys Asp Phe Cys
      20                      25                      30
Lys Asp Phe
      35

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

```

Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1      5                      10                      15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys

```

SUBSTITUTE SHEET (RULE 26)

485

```

      20      25      30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
      35      40      45
Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
      50      55      60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
      65      70      75      80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
      85      90      95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
      100      105      110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
      115      120      125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
      130      135      140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
      145      150      155      160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
      165      170      175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
      180      185      190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
      195      200      205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
      210      215      220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
      225      230      235      240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
      245      250      255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
      260      265      270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
      275      280      285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
      290      295      300
Tyr Leu Ala
      305

```

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

```

Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1      5      10      15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys
      20      25      30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
      35      40      45

```

SUBSTITUTE SHEET (RULE 26)

486

```

Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
 50          55          60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
 65          70          75          80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
          85          90          95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
          100          105          110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
          115          120          125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
          130          135          140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
          145          150          155          160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
          165          170          175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
          180          185          190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
          195          200          205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
          210          215          220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
          225          230          235          240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
          245          250          255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
          260          265          270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
          275          280          285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
          290          295          300
Tyr Leu Ala
          305

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

```

Val Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser
 1          5          10          15
Ile Gln Ser Asp Ser Gln Tyr Leu Gln Ala Unk Leu Asn Gln Phe Glu
          20          25          30
Asn Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr
          35          40          45
His Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His
          50          55          60
Ala Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe

```

SUBSTITUTE SHEET (RULE 26)

487

65		70		75		80									
Leu	Gln	Glu	Thr	Leu	Lys	Ser	Leu	Glu	Ile	Gln	Leu	Lys	Asn	Tyr	Ala
		85						90						95	
Pro	Lys	Leu	Leu	Asn	Ser	Lys	Glu	Val	Leu	Asn	Phe	Tyr	Ala	Glu	Tyr
		100						105						110	
Ile	Asn	Gly	Phe	Glu	Leu	Pro	Leu	Lys	Pro	Leu	Val	Gly	Gly	Tyr	Leu
		115						120						125	
Ser	Asp	Ser	Tyr	Ile	Ala	Ser	Ser	Ile	Thr	Phe	Glu	Lys	Asp	Tyr	Phe
		130						135						140	
Ile	Gln	Glu	Ser	Phe	Asn	Gln	Lys	Thr	Tyr	Asn	Arg	Leu	Ile	Gly	Ile
		145						150						155	
Lys	Ala	Tyr	Glu	Ser	Glu	Arg	Ile	Thr	Ser	Ile	Ala	Val	Gly	Ala	Leu
								165						170	
Leu	Tyr	Gln	Glu	Thr	Pro	Leu	Asp	Ile	Ile	Phe	Ser	Ile	Glu	Pro	Met
								180						185	
Ser	Val	Asn	Lys	Thr	Leu	Ser	Phe	Leu	Lys	Glu	Arg	Ala	Lys	Phe	Ser
								195						200	
Met	Ser	Asn	Leu	Val	Lys	Asn	Glu	Leu	Leu	Glu	Tyr	Gln	Glu	Leu	Val
								210						215	
Lys	Thr	Lys	Arg	Leu	Ser	Met	Gln	Lys	Phe	Ala	Leu	Asn	Val	Leu	Ile
								225						230	
Lys	Ala	Pro	Ser	Leu	Glu	Asp	Leu	Asp	Ala	Gln	Thr	Ser	Leu	Ile	Leu
								235						240	
Gly	Leu	Leu	Phe	Lys	Glu	Asn	Leu	Val	Gly	Val	Ile	Glu	Thr	Phe	Gly
								245						250	
Leu	Lys	Gly	Tyr	Phe	Ser	Phe	Phe	Pro	Glu	Arg	Ile	His	Leu	Asn	
								255						260	
His	Arg	Leu	Arg	Phe	Leu	Thr	Ser	Lys	Ala	Leu	Ala	Cys	Leu	Met	Val
								265						270	
Phe	Glu	Arg	Gln	Asn	Leu	Gly	Phe	Lys	Ala	Asn	Ser	Trp	Gly	Asn	Ser
								275						280	
Pro	Leu	Ser	Val	Phe	Lys	Asn	Leu	Asp	Tyr	Ser	Pro	Phe	Leu	Phe	Asn
								285						290	
Phe	His	Asn	Gln	Glu	Val	Ser	His	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Arg
								295						300	
Val	Asn	Gly	His	Thr	Leu	Val	Ile	Gly	Ala	Thr	Gly	Ser	Gly	Lys	Ser
								305						310	
Thr	Leu	Ile	Ser	Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Gln	Asn	Met
								315						320	
Arg	Leu	Leu	Ala	Phe	Asp	Arg	Met	Gln	Gly	Leu	Tyr	Ser	Phe	Thr	Glu
								325						330	
Phe	Phe	Lys	Gly	His	Tyr	His	Asp	Gly	Gln	Ser	Phe	Ser	Ile	Asn	Pro
								335						340	
Phe	Cys	Leu	Glu	Pro	Asn	Leu	Gln	Asn	Leu	Glu	Phe	Leu	Gln	Ser	Phe
								345						350	
Phe	Leu	Ser	Met	Leu	Asp	Leu	Ala	Pro	Ser	Arg	Asp	Lys	Glu	Ala	Leu
								355						360	
Glu	Asp	Met	Asn	Ala	Ile	Ser	Gly	Ala	Ile	Lys	Ser	Leu	Tyr	Glu	Thr
								365						370	
Leu	Tyr	Pro	Lys	Asp	Phe	Ser	Leu	Leu	Asp	Phe	Lys	Glu	Thr	Leu	Lys
								375						380	
Arg	Thr	Ser	Ser	Asn	Gln	Leu	Gly	Leu	Ser	Leu	Glu	Pro	Tyr	Leu	Asn
								385						390	
Asn	Pro	Leu	Phe	Asn	Ala	Leu	Asn	Asp	Ala	Phe	Asn	Ser	Asn	Ala	Phe
								395						400	
Leu	Asn	Val	Ile	Asn	Leu	Asp	Ala	Ile	Thr	Gln	Asn	Pro	Lys	Asp	Leu
								405						410	
Gly	Leu	Leu	Ala	Tyr	Tyr	Leu	Phe	Tyr	Lys	Ile	Leu	Glu	Glu	Ser	Arg
								415						420	
Lys	Asn	Asp	Ser	Gly	Phe	Leu	Val	Phe	Leu	Asp	Glu	Phe	Lys	Ser	Tyr
								425						430	
Val	Glu	Asn	Asp	Leu	Leu	Asn	Thr	Lys	Ile	Asn	Ala	Leu	Ile	Thr	Gln
								435						440	
Ala	Arg	Lys	Ala	Asn	Gly	Val	Val	Val	Leu	Ala	Leu	Gln	Asp	Ile	Tyr
								445						450	
								455						460	
								465						470	
								475						480	
								485						490	
								495						500	
								505						510	
								515						520	
								525						530	
								535						540	
								545						550	
								555						560	
								565						570	
								575						580	
								585						590	

SUBSTITUTE SHEET (RULE 26)

488

Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
 595 600 605
 Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
 610 615 620
 Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
 625 630 635 640
 Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
 645 650 655
 Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
 660 665 670
 Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
 675 680 685
 Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
 690 695 700

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586

Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser
 1 5 10 15
 Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala
 20 25 30
 Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Unk
 35 40 45
 Tyr Leu Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile
 50 55 60
 Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala
 65 70 75 80
 Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln
 85 90 95
 Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp
 100 105 110
 Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn
 115 120 125
 Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile
 130 135 140
 Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu
 145 150 155 160
 Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala
 165 170 175
 Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg
 180 185 190
 Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg
 195 200 205
 Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn
 210 215 220
 Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys

SUBSTITUTE SHEET (RULE 26)

489

```

225          230          235          240
Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
          245          250          255
Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
          260          265          270
Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
          275          280          285
Asn Lys Lys Gln Phe
          290

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

```

Met Pro Lys Ser Phe Thr Leu Pro Thr Phe Val Trp Cys Leu Phe Val
1          5          10          15
Gly Val Ile Leu Arg Asn Ala Leu Ser Phe Phe Lys Ile His Ser Val
          20          25          30
Phe Asp Arg Glu Val Ser Val Ile Gly Asn Val Ser Leu Ser Leu Phe
          35          40          45
Leu Ala Tyr Ala
          50

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588

```

Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile Leu
1          5          10          15
Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu Ser
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

490

```

Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys Ala
    35              40              45
Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu Val
    50              55              60
Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser Gly
    65              70              75              80
Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys Pro
    85              90              95
Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser Ile
    100             105             110
Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln Asp
    115             120             125
Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala Phe
    130             135             140
Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr Gly
    145             150             155             160
Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys Arg
    165             170             175
Leu Leu Glu Ser Arg Leu
    180

```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

```

Val Ser Leu Ile Lys Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser
1      5              10              15
Ile Pro Leu Thr Ser Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His
    20              25              30
Ala Phe Ser Asp Tyr Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe
    35              40              45
Ser Leu Lys His Tyr Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile
    50              55              60
Lys Asp Lys Glu Lys Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr
    65              70              75              80
His Phe Leu Gly Ala Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser
    85              90              95
Glu Met Ile Tyr Tyr Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn
    100             105             110
Leu Glu Asn Thr Leu Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu
    115             120             125
Asp Asn Phe Met Ile Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly
    130             135             140
Gly Met Asp Phe Glu Leu Ser Arg Ile Ser Tyr Pro Leu Leu Ile His
    145             150             155             160
Ser Phe Asp Asp Asn Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln
    165             170             175
Tyr Gly Ser Lys Thr Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu

```

SUBSTITUTE SHEET (RULE 26)

491

```

      180              185              190
Glu Leu Lys Thr Ala Thr Pro Leu Leu Asn Arg Thr Ala Met Pro Lys
      195              200              205
Glu His Ala Leu Leu Ile Ile His Glu Thr Asn Ala Leu Val Phe Leu
      210              215              220
Glu Met Leu Lys Ile Phe Gly Leu Leu Ser Gln Val His His Asn Asp
      225              230              235              240
Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn
      245              250

```

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

```

Val Ile Thr Ala Cys Phe Asn Arg Glu Lys Thr Ile Glu Asp Thr Ile
1           5           10           15
Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile Glu Tyr Ile Ile Ile
      20           25           30
Asp Gly Ala Ser Ala Ile Ala Leu
      35           40

```

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591

```

Val Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe
1           5           10           15
Glu Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr
      20           25           30
Ile Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala
      35           40           45

```

SUBSTITUTE SHEET (RULE 26)

492

```

Arg Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys
 50          55          60
Glu Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn
65          70          75          80
Gly Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys
      85          90          95
Tyr Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Glu
      100         105         110
Lys Leu His Val Trp Leu Cys Gln Ile Tyr
      115         120

```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592

```

Met Lys Arg Leu Ala Val Ala Leu Ile Leu Val Leu Gly Val Val Trp
 1          5          10          15
Gly Lys Ser Leu Pro Lys Trp Ala Lys Asp Cys Ser Lys Glu Met Arg
      20          25          30
Ile Glu Lys Thr Gln Thr Lys Asp Glu Lys Ile Leu Val Cys Gly Met
      35          40          45
Ser Asp Ile Leu Leu Ser Asp Met Asp Tyr Ser Leu Ser Ser Ala Arg
      50          55          60
Gln Asn Ala Leu Glu Lys Val Met Glu Ala Phe Lys Gly Asp Arg Ile
      65          70          75          80
Glu Ile Lys Ala Gly Glu Leu Lys Ala Thr Phe Ile Asp Thr Asp Lys
      85          90          95
Val Tyr Val Leu Leu Arg Ile Thr Lys Lys His Val Ala Leu Met Asn
      100         105         110
Glu

```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

493

(A) NAME/KEY: misc_feature
(B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

```

Met Asn Pro Gln Ile Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu
1      5      10      15
Leu Ala Ala Ser Gly Asn Leu Val Glu Trp Tyr Asp Phe Tyr Ala
20      25      30
Tyr Ala Phe Leu Ala Pro Tyr Phe Ala Lys Glu Phe Thr His Thr Asn
35      40      45
Asp Pro Thr Leu Ala Leu Ile Ser Ala Phe Leu Val Phe Met Leu Gly
50      55      60
Phe Phe Met Arg Pro Leu Gly Ser Leu Phe Phe Gly Lys Leu Gly Asp
65      70      75      80
Lys Lys Gly Arg Lys Thr Ser Met Val Tyr Ser Ile Ile Leu Met Ala
85      90      95
Leu Gly Ser Phe Met Leu Ala Leu Leu Pro Thr Lys Glu Ile Val Gly
100     105     110
Glu Trp Ala Phe Leu Phe Leu Leu Ala Arg Leu Leu Gln Gly Phe
115     120     125
Ser Val Gly Gly Glu Tyr Gly Val Val Ala Thr Tyr Leu Ser Glu Leu
130     135     140
Gly Lys Asn Gly Lys Lys Gly Phe Tyr Gly Ser Phe Gln Tyr Val Thr
145     150     155     160
Leu Val Gly Gly Gln Leu Leu Ala Ile Phe Ser Leu Phe Ile Val Glu
165     170     175
Asn Val Tyr Thr His Glu Gln Ile Ser Ala Phe Ala Trp Arg Tyr Leu
180     185     190
Phe Ala Leu Glu Gly Ile Leu Ala Leu Leu Ser Leu Phe Leu Arg Asn
195     200     205
Ile Met Glu Glu Thr Met Asp Asn Glu Ala Thr Pro Gln Lys Lys Thr
210     215     220
Asn Val Asn Asn Thr Lys Glu Thr His Ile Lys Glu Thr Gln Arg Gly
225     230     235     240
Ser Leu Lys Glu Leu Leu Asn His Lys Lys Ala Leu Met Ile Val Phe
245     250     255
Gly Leu Thr Met Gly Gly Ser Leu Cys Phe Tyr Thr Phe Thr Val Tyr
260     265     270
Leu Lys Ile Phe Leu Thr Asn Ser Ser Ser Phe Ser Pro Lys Glu Ser
275     280     285
Ser Phe Ile Met Leu Leu Ala Leu Ser Tyr Phe Ile Phe Leu Gln Pro
290     295     300
Leu Cys Gly Met Leu Ala Asp Lys Ile Lys Arg Thr Gln Met Leu Met
305     310     315     320
Val Phe Ala Ile Thr Gly Leu Ile Val Thr Pro Ile Val Phe Tyr Gly
325     330     335
Ile Lys His Ala Thr Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu
340     345     350
Ala Leu Ser Ser Met Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys
355     360     365
Ala Glu Leu Phe Pro Glu His Val Arg Ala Leu Gly Val Gly Leu Ala
370     375     380
Tyr Ala Ile Ala Asn Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala
385     390     395     400
Leu Glu Phe Lys Gln His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val
405     410     415
Met Leu Ser Ile Val Ile Phe Met Val Met Val Ile Ile Phe Pro Lys
420     425     430
Lys Thr Tyr Leu Glu
435

```

(2) INFORMATION FOR SEQ ID NO:594:

SUBSTITUTE SHEET (RULE 26)

494

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1      5      10      15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20      25      30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu
35      40      45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
50      55      60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
65      70      75      80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
85      90      95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
100     105     110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu
115     120     125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
130     135     140
Lys Ala
145

```

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1      5      10      15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20      25      30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu

```

SUBSTITUTE SHEET (RULE 26)

495

```

      35      40      45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
  50      55      60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
  65      70      75      80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
      85      90      95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
      100      105      110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu
      115      120      125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Ala
      130      135      140
Lys Ala
      145

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
  1      5      10      15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
      20      25      30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
      35      40      45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
      50      55      60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
      65      70      75      80
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
      85      90      95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
      100      105      110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
      115      120      125

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

496

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

```

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1      5      10      15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
      20      25      30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
      35      40      45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
      50      55      60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
      65      70      75      80
Lys Ala Leu Glu Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
      85      90      95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
      100     105     110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe
      115     120     125
  
```

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

```

Met Asp Ile Ser Ile Phe Arg Glu Tyr Asp Ile Arg Gly Ile Tyr Pro
1      5      10      15
Thr Thr Leu Asp Glu Asn Thr Ala Phe Ser Ile Gly Val Glu Leu Gly
      20      25      30
Lys Ile Met Arg Glu Tyr Asp Lys Ser Val Phe Val Gly His Asp Ala
      35      40      45
Arg Val His Gly Arg Phe Leu Phe Glu Val Leu Ser Ala Gly Leu Gln
      50      55      60
Ser Ser Gly Leu Lys Val Tyr Asp Leu Gly Leu Ile Pro Thr Pro Val
      65      70      75      80
Ala Tyr Phe Ala Ala Phe Asn Glu Ile Asp Asn Ile Gln Trp Pro
      85      90      95
  
```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

497

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

```

Val Cys Asp Ile Phe Ser Asp Gly Val Leu Leu Asp Lys Ala Leu Val
1      5      10      15
Ile Tyr Phe Lys Ala Pro Tyr Ser Phe Thr Gly Glu Asp Val Cys Glu
20     25     30
Ile Gln Cys His Gly Ser Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala
35     40     45
Cys Leu Asn Leu Gly Ala Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys
50     55     60
Lys Ala Phe Leu Asn His Lys Met Asp Leu Ser Glu Ile Glu Ala Ser
65     70     75     80
Val Gln Leu Ile Leu Cys Glu Asp Glu Ser Val Leu Asn Ala Leu Ala
85     90     95
Arg Gln Leu Gln Gly Gly
100
  
```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

```

Met Phe Lys Lys Met Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys
1      5      10      15
Val Gly Ala Lys Asp Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly
20     25     30
Gly Lys Phe Met Gly Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr
35     40     45
Ser Met Asn Asp Glu Pro Val Ile Lys Asn Leu Ile Val Asn Arg
50     55     60
Gly Asn Ser Val Glu Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp
65     70     75     80
Lys Phe Lys Lys Glu Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln
85     90     95
  
```

SUBSTITUTE SHEET (RULE 26)

498

Gln Ile Phe Tyr Arg Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val
 100 105 110
 Lys Ile Ile Thr Asp Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

Met Thr Leu Lys Pro Tyr Pro Thr Lys Glu Thr Gly Leu Ala Ser Gln
 1 5 10 15
 Leu Ser Gly His Trp Phe Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn
 20 25 30
 Phe Asn Pro Asn Lys Ile Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser
 35 40 45
 Lys Ile Lys Phe Asp Lys Asp Leu Glu Ile Tyr Phe Asp Ser His Glu
 50 55 60
 Ser Phe Asn Ile Ser Lys Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser
 65 70 75 80
 Leu Lys Lys Ile Lys Gln Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile
 85 90 95
 Glu Ser Lys His Asp Asn Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu
 100 105 110
 Asn Asp Thr Ser Phe Leu Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu
 115 120 125
 Glu Tyr Asn Met Gln Leu Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe
 130 135 140
 Asn Lys Leu Leu Ala Ile Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln
 145 150 155 160
 Leu Lys Ile Arg Val Arg His Asn Asn Lys Leu Pro Arg Glu Lys Tyr
 165 170 175
 Thr Glu His Glu Ile Lys Leu Glu Val Tyr Asp Cys Arg Lys Ser His
 180 185 190
 Asp His Asn Glu Pro Ile Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln
 195 200 205
 Trp Ala Phe Asn Phe Met Phe Gly Phe Leu Tyr Asn Val Gly Ser His
 210 215 220
 Phe Ser Phe Asn His Asn Ile Ile Tyr Val Met Asp Glu Pro Ala Thr
 225 230 235 240
 His Leu Ser Val Pro Ala Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu
 245 250 255
 Tyr Ala His Lys Asn His Val Thr Phe Val Leu Ala Thr His Asp Pro
 260 265 270
 Phe Leu Val Asp Thr Asp His Leu Asp Glu Ile Arg Ile Val Glu Lys
 275 280 285
 Glu Thr Glu Gly Ser Val Ile Lys Asn His Phe Asn Tyr Pro Leu Asn
 290 295 300
 Asn Ala Ser Lys Asp Ser Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu

SUBSTITUTE SHEET (RULE 26)

499

```

305          310          315          320
Gly Val Gly Gln His Val Phe His Asn Pro Gln Lys His Arg Ile Ile
          325          330          335
Phe Val Glu Gly Ile Thr Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu
          340          345          350
Tyr Leu Arg Tyr Lys Glu Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe
          355          360          365
Leu Pro Ile Ser Gly Leu Lys Asn Asp Ser Asn Asp Met Lys Glu Thr
          370          375          380
Ile Glu Lys Leu Cys Glu Leu Asp Asn His Pro Ile Val Leu Thr Asp
385          390          395          400
Asp Asp Arg Lys Cys Val Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe
          405          410          415
Lys Arg Ala Asn Glu Glu Met His Asp Pro Ile Thr Ile Leu Gln Leu
          420          425          430
Ser Asp Cys Asp Arg His Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala
          435          440          445
Asn Asp Arg Asn Lys Tyr Ala Lys Asn Lys Gln Met Glu Leu Ser Met
          450          455          460
Ala Phe Lys Thr Arg Leu Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys
465          470          475          480
Gln Thr Lys Arg Asn Phe Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala
          485          490          495
Thr Asn Leu Ile Lys Asn
          500

```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

```

Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1          5          10          15
Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
          20          25          30
Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
          35          40

```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

500

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

```

Met Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala
1      5      10      15
Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys
      20      25      30
Asp Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn
      35      40      45
Ile Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr
      50      55      60
Phe Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu
      65      70      75      80
Phe Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr
      85      90      95
Ser Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr
      100     105     110
Asn Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr
      115     120     125
Asn Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln
      130     135     140
Asn Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr
      145     150     155     160
Lys Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser
      165     170     175
Leu Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu
      180     185     190
Ile Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr
      195     200     205
Ile Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu
      210     215     220
Glu Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile
      225     230     235     240
Lys Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr
      245     250     255
Leu Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln
      260     265     270
Glu Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln
      275     280     285
Ile Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn
      290     295     300
Thr Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe
      305     310     315     320
Glu Leu Glu Lys Glu Ser Ala Ser Asp Phe Ile Arg His Ser Tyr Ser
      325     330     335
Met Leu Glu Lys Ala
      340

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

501

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

```

Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys Cys Ala Phe Leu
1      5      10      15
Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His Ser Lys Gly Leu
      20      25      30
His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro Asn Leu Phe Ser
      35      40      45
Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro Val Glu Glu Ser
      50      55      60
Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr Val Val Lys Thr
      65      70      75      80
Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro Ile Glu Trp Ala
      85      90      95
Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp Asn Ser Lys Glu
      100      105      110
Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu Ser Ser Arg Val
      115      120      125
Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile Thr Lys Arg Tyr
      130      135      140
Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu Phe Phe Ile Lys
      145      150      155      160
Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys Glu Leu Lys Glu
      165      170      175
Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu Thr His Lys Lys
      180      185      190
Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr Asp His Leu Lys
      195      200      205
Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly Gly Leu Val Arg
      210      215      220
Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe Lys Leu Tyr Asn
      225      230      235      240
Lys Leu Pro Phe Glu Ser Ile Asn Asn Glu Asn Thr Lys Leu Asn Thr
      245      250      255
Asn Asp Asn Glu Glu Val Lys Lys Leu Glu Phe Glu Leu Ala Lys Glu
      260      265      270
Val His Ile Leu Ile Leu Glu Gln Gln Leu Leu Ser Ala Thr Asn Tyr
      275      280      285
Tyr Ser Trp Ile Asp Lys Asp Asp Asn Ala Asn Phe Ala Trp Lys Met
      290      295      300
His Arg Leu Ile Asn Glu Asn Lys Leu Lys Glu Asn His Leu Ser Ala
      305      310      315      320
Asn Asn Ala Asn Lys Ile Lys Gln Phe Phe Phe Asn Asn Gly Ser Ile
      325      330      335
Leu Gly Trp Thr Lys Glu Glu Gln Ser Ala Ile Gln Glu Asn Arg Asp
      340      345      350
Tyr Ser Leu Arg Ser Ala Leu Leu Ser Leu Glu Glu Ile Ala Gln Ala
      355      360      365
Lys Ile Glu Leu Gln Lys Tyr Tyr Glu Ser Val Tyr Val Asn Gly Asp
      370      375      380
Gly Asn Lys Arg Glu Ile Lys Pro Phe Lys Glu Ile Leu Arg Asp Thr
      385      390      395      400
Asn Asn Phe Glu Lys Ala Tyr Lys Glu Arg Tyr Asp Lys Leu Val Ser
      405      410      415
Leu Ser Ala Ala Ile Ile Gln Ala Lys Glu Gly Gly Asn Glu Arg Gln
      420      425      430

```

SUBSTITUTE SHEET (RULE 26)

502

Asn Ser Ser Ala Asn Asn Asn Asn Pro Ile Lys Asn Thr Ile Glu Thr
 435 440 445
 Asn Thr Ser Asn Asn Ile Ile Gln Asn Asn Asp Asn Ile Ile Ile Gln
 450 455 460
 Ile
 465

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603

Met Ala Leu Glu Val Val Leu Trp Asp Phe Asp Gly Val Ile Phe Asp
 1 5 10 15
 Ser Met His Leu Lys Tyr Glu Gly Phe Lys Ala Leu Phe Gln Lys His
 20 25 30
 Gly Asn Asp Ser Lys Glu Gly Leu Lys Gln Phe Glu Val Tyr His Tyr
 35 40 45
 Gln Ser Gly Gly Ile Ser Arg Asn Glu Lys Ile Gln Tyr Phe Tyr Asn
 50 55 60
 Glu Ile Leu Lys Thr Pro Ile Ala Gln Glu Glu Ile Asp Ala Leu Ala
 65 70 75 80
 Leu Glu Phe Gly Ala Ile Ile Glu Gln Lys Leu Phe Asp Arg Gly His
 85 90 95
 Leu Asn Ser Glu Val Met Ala Phe Ile Asp Lys His Tyr Gln Asn Tyr
 100 105 110
 Ile Phe His Ile Ala Ser Ala Ala Leu His Ser Glu Leu Gln Val Leu
 115 120 125
 Cys Glu Phe Leu Gly Ile Thr Lys Tyr Phe Lys Ser Val Glu Gly Ser
 130 135 140
 Pro Pro Asp Lys Pro Lys Ile Ile Ala Asn Ile Ile Gln Lys Tyr Ala
 145 150 155 160
 Tyr Asp Pro Ser Arg Met Leu Met Ile Ala Ile Ala Ser Met Ile Met
 165 170 175
 Lys Ala Leu Arg Leu Ile Lys Trp Arg Phe Trp Ala Ile Thr Ala Arg
 180 185 190
 Phe

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

503

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604

```

Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1           5           10           15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
20           25           30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
35           40           45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
50           55           60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65           70           75           80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
85           90           95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
100          105          110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Gln Phe Phe Gly Ser Asn Asp
115          120          125
Ala Leu Leu Asn Met Ser Asn Ala Ile Leu Lys Ser Phe
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605

```

Val Lys Cys Leu Leu Ile Lys Lys Ser Leu Leu Phe Ala Leu Lys Pro
1           5           10           15
Leu Pro Asp Leu Lys Thr Thr Thr Pro Ile Leu Ala Pro Met Ser Val
20           25           30
Val Ala Gly Arg Leu Unk Unk His Leu Val Gln His Tyr Leu Leu Ala
35           40           45
Leu Glu His Val Lys Gly Phe Met Gly Lys Gly Val Ile Leu Gly Gly
50           55           60
Leu Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val
65           70           75           80
Val Gly Met Glu Ser Ala Lys Val Leu Unk Gln Met Gly Unk Lys Val
85           90           95
Thr Ile Leu Glu Leu Asp Tyr Ala Lys Leu Gln Asn His Pro Tyr Tyr
100          105          110

```

SUBSTITUTE SHEET (RULE 26)

504

```

His Leu Tyr Asp Leu Glu Val Leu Ser Val Asn Glu Ala Asn Ile Ile
   115           120           125
Gln Ala Leu Asn Gly Unk Val Gly Leu Val Gly Ala Val Leu Val Thr
   130           135           140
Unk Ser Gln Thr Pro Lys Val Unk Leu Arg Arg His Leu Lys Tyr
145           150           155

```

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606

```

Met Leu Ala Lys Ile Val Phe Ser Ser Leu Val Ala Phe Gly Val Leu
1           5           10           15
Ser Ala Asn Val Glu Gln Phe Gly Ser Phe Phe Asn Glu Ile Lys Lys
   20           25           30
Glu Gln Glu Val Ala Ala Lys Glu Asp Ala Leu Lys Ala Arg Lys
   35           40           45
Lys Leu Leu Asn Asn Thr His Asp Phe Leu Glu Asp Leu Val Phe Arg
   50           55           60
Lys Gln Lys Ile Lys Glu Leu Val Asp Tyr Arg Ala Lys Val Leu Leu
65           70           75           80
Asp Leu Glu Asn Lys Tyr Lys Lys Glu Lys Glu Ala Leu Glu Lys Glu
   85           90           95
Thr Arg Gly Lys Ile Leu Thr Ala Lys Ser Lys Ala Tyr Gly Asp Leu
100          105          110
Glu Gln Ala Leu Lys Asp Asn Pro Leu Tyr Lys Lys Leu Leu Pro Asn
115          120          125
Pro Tyr Ala Tyr Val Leu Asn Gln Glu Thr Phe Thr Gln Glu Asp Lys
130          135          140
Glu Arg Leu Ser Tyr Tyr Tyr Pro Gln Val Lys Thr Ser Ser Ile Phe
145          150          155          160
Lys Lys Thr Thr Ala Thr Thr Lys Asp Lys Ala Gln Ala Leu Leu Gln
165          170          175
Met Gly Val Phe Ser Leu Asp Glu Glu Gln Asn Lys Lys Ala Ser Arg
180          185          190
Leu Ala Leu Ser Tyr Lys Gln Ala Ile Glu Glu Tyr Ser Asn Asn Ile
195          200          205
Ser Asn Leu Leu Ser Arg Lys Glu Leu Asp Asn Ile Asp Tyr Tyr Leu
210          215          220
Gln Leu Glu Arg Asn Lys Phe Asp Ser Lys Ala Lys Asp Ile Ala Gln
225          230          235          240
Lys Ala Thr Asn Thr Leu Ile Phe Asn Ser Glu Arg Leu Ala Phe Ser
245          250          255
Met Ala Ile Asp Lys Ile Asn Glu Lys Tyr Leu Arg Gly Tyr Glu Ala
260          265          270
Phe Ser Asn Leu Leu Lys Asn Val Lys Asp Asp Val Glu Leu Asn Thr
275          280          285
Leu Thr Lys Asn Phe Thr Asn Gln Lys Leu Ser Phe Ala Gln Lys Gln

```

SUBSTITUTE SHEET (RULE 26)

505

290	295	300
Lys Leu Cys Leu Leu Val	Leu Asp Ser Phe Asn Phe Asp Thr Gln Ser	
305	310	315
Lys Lys Ser Ile Leu Lys	Lys Thr Asn Glu Tyr Asn Ile Phe Val Asp	320
	325	330
Ser Asp Pro Met Met Ser Asp	Lys Thr Thr Met Gln Lys Glu His Tyr	335
	340	345
Lys Ile Phe Asn Phe Phe Lys	Thr Val Val Ser Ala Tyr Arg Asn Asn	350
	355	360
Val Ala Lys Asn Asn Pro Phe	Glu	365
370	375	

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607

Met	Asp	Phe	Val	Gly	Phe	Glu	Asp	Leu	Lys	Cys	Lys	Asp	Lys	Glu	Asn
1			5					10						15	
Ser	Gln	Lys	Val	Phe	Val	Ile	Arg	Asn	Asp	Lys	Leu	Gly	Asp	Phe	Ile
		20					25					30			
Leu	Glu	Ile	Pro	Ala	Leu	Ile	Ala	Leu	Lys	His	Ala	Phe	Leu	Glu	Lys
	35					40					45				
Gly	Val	Glu	Val	Tyr	Leu	Gly	Val	Val	Val	Pro	Ser	Tyr	Thr	Thr	Pro
	50				55					60					
Ile	Ala	Leu	Glu	Phe	Pro	Phe	Ile	Asp	Glu	Val	Ile	Ile	Glu	Asp	Asn
65				70					75					80	
His	Leu	Ala	Thr	Thr	His	Lys	Asn	Arg	Ser	Ile	Asp	Ala	Leu	Ile	Phe
		85						90					95		
Leu	Phe	Ser	Asn	Phe	Lys	Asn	Ala	Lys	Leu	Ala	Phe	Ser	Leu	Arg	Lys
		100					105						110		
Ser	Ile	Pro	Tyr	Ile	Leu	Ala	Pro	Lys	Thr	Lys	Ile	Tyr	Ser	Trp	Leu
	115					120						125			
Tyr	Gln	Lys	Arg	Val	Arg	Gln	Asn	Arg	Ser	Leu	Cys	Leu	Lys	Thr	Glu
	130				135					140					
Tyr	Glu	Tyr	Asn	Leu	Asp	Leu	Ile	His	Ala	Phe	Cys	Lys	Asp	Tyr	Asp
145			150						155					160	
Leu	Pro	Asn	Ala	Gln	Leu	Lys	Lys	Ile	Ala	Trp	Lys	Leu	Lys	Asp	Lys
		165					170						175		
Ser	Lys	Glu	Arg	Ser	Ile	Ile	Ala	Ser	Lys	Leu	Asn	Ala	Asn	Val	Asp
	180						185						190		
Leu	Leu	Trp	Ile	Gly	Val	His	Met	His	Ser	Gly	Gly	Ser	Ser	Pro	Val
	195					200						205			
Leu	Pro	Ala	Ser	His	Phe	Ile	Glu	Leu	Ile	Ala	Ile	Leu	His	Glu	Lys
	210				215						220				
Leu	Ser	Cys	Glu	Ile	Ile	Leu	Ile	Cys	Gly	Pro	Gly	Glu	Arg	Lys	Ala
225			230						235					240	
Thr	Glu	Glu	Leu	Leu	Lys	Glu	Val	Pro	Phe	Ala	His	Leu	Tyr	Asp	Thr
			245					250						255	

SUBSTITUTE SHEET (RULE 26)

506

```

Ser His Ser Leu Val Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val
      260      265      270
Cys Ile Gly Asn Ala Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp
      275      280      285
Asn Gln Ser Ile Gly Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala
      290      295      300
Arg Trp Arg Pro Phe Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn
      305      310      315      320
Gly Ser Asn Asp Met Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys
      325      330      335
Ile Met Gly Phe Ile Thr Lys Asn Leu Ser His His Met Gln Glu Arg
      340      345      350

```

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608

```

Val Gly Val Leu Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly
1      5      10      15
Leu Cys Val Leu Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala
      20      25      30
Tyr Tyr Leu Met Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu
      35      40      45
Ile Lys Asn Arg Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro
      50      55      60
Ile His Gln Thr Cys Gln Ser Thr Gln Phe Leu Ser Pro Cys Val Arg
      65      70      75      80
Leu Val Phe Ser Pro Ile Gly Arg
      85

```

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

SUBSTITUTE SHEET (RULE 26)

507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

```

Met Ser Leu Gly Ala Val Val Ser Ser Leu Leu Cys His Lys Leu Glu
1          5          10          15
Gly Ala Ile Leu Asp Leu Arg Ala Tyr Arg Unk Unk Ala Tyr Tyr His
          20          25          30
Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu Leu Tyr
          35          40          45
Asn Tyr Ile Lys Ala His Ile Unk Leu Asn Leu Leu Trp Thr Ile Arg
50          55          60
Asn Arg Thr Unk Ser Leu Gly Lys Phe Thr Gln Asn Pro Thr Glu Gln
65          70          75          80
Pro Pro Thr Asn Asn His
          85

```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610

```

Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser
1          5          10          15
Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu Asn
          20          25          30
Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys Leu
          35          40          45
Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu
50          55          60
His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

508

(B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611

```

Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1      5      10      15
Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
20      25      30
Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
35      40      45
Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
50      55      60
Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65      70      75      80
Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
85      90      95
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

```

Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1      5      10      15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
20      25      30
Ile Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu
35      40      45
Asn Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu
50      55      60
Leu Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro
65      70      75      80
Ser Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile
85      90      95
Leu His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg
100      105      110
Arg Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu
115      120      125
Cys Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu
130      135      140
Trp Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly
145      150      155      160
Ser Ala

```

(2) INFORMATION FOR SEQ ID NO:613:

SUBSTITUTE SHEET (RULE 26)

509

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

Val	Ile	Met	Thr	Lys	Leu	Asp	Gly	Thr	Ser	Lys	Gly	Gly	Ala	Ile	Leu
1				5				10					15		
Unk	Val	Leu	Tyr	Glu	Leu	Lys	Leu	Pro	Ile	Leu	Tyr	Leu	Gly	Met	Gly
		20				25						30			
Glu	Lys	Glu	Asp	Asp	Leu	Ile	Ala	Phe	Asp	Glu	Glu	Arg	Phe	Ile	Glu
		35				40						45			
Asp	Leu	Val	Asp	Ala	Val	Phe	Val	Glu	Gln						
	50					55									

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614

Val	Cys	Gly	Ala	His	Gly	Lys	Ser	Ser	Ile	Thr	Unk	Met	Leu	Ser	Ala
1				5					10				15		
Ile	Cys	Pro	Ala	Phe	Gly	Unk	Ile	Ile	Gly	Arg	His	Ser	Lys	Glu	Phe
		20				25						30			
Asp	Ser	Asn	Val	Unk	Glu	Ser	Ala	Asp	Met	Ser	Leu	Val	Phe	Glu	Unk
		35				40					45				
Asp	Glu	Ser	Asp	Ser	Ser	Phe	Phe	Ile	Phe	Gln	Pro	Phe	Leu	Arg	Asp
	50					55					60				
Cys	Ala														
65															

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids

SUBSTITUTE SHEET (RULE 26)

510

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10           15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
          20           25           30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
          35           40           45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
          50           55           60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
          65           70           75           80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu
          85           90           95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
          100          105          110
Unk Leu Gly Pro
          115

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10           15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
          20           25           30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
          35           40           45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
          50           55           60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
          65           70           75           80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu

```

SUBSTITUTE SHEET (RULE 26)

511

```

      85          90          95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
      100          105          110
Unk Leu Gly Pro
      115

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

```

Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln
1          5          10          15
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
      20          25          30
Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
      35          40          45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
      50          55          60
Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
      65          70          75          80
Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

```

Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln
1          5          10          15
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
      20          25          30

```

SUBSTITUTE SHEET (RULE 26)

512

Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
 35 40 45
 Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
 50 55 60
 Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
 65 70 75 80
 Ala Phe

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617

Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Gly Asn Gly Lys Ala
 1 5 10 15
 Asp Leu Ser Asn Glu Asn Thr Lys Val Arg Gln Thr Lys Thr Asn Leu
 20 25 30
 Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu Lys Thr Glu Leu Asn Asn
 35 40 45
 Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu Arg Leu Ala Ala Asp Lys
 50 55 60
 Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg Lys Pro Asn
 65 70 75

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618

Met Asp Leu Gln Gln Ile Asp Glu Leu Glu Asn Lys Phe Glu Glu Gln
 1 5 10 15
 Glu Glu Gln Ala Gln Asp Thr Pro Leu Lys Gln Glu Pro Ser Thr Lys

SUBSTITUTE SHEET (RULE 26)

513

```

      20      25      30
Glu Val Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Ser Leu Leu Asp
      35      40      45
Glu Asp Lys Lys Lys Ser Phe Asn Ile Ala Phe Ser Pro Cys Val Ile
      50      55      60
Lys Glu Leu Asn Glu Phe Leu Leu Glu Phe Gly Ser Phe Lys Glu Thr
      65      70      75      80
Arg Ser Thr Phe Ile Glu Glu Ala Leu Ile Arg His Leu Lys His Arg
      85      90      95
Lys Asn Thr Gln Glu Gln Lys Leu Leu Lys Gln Leu Glu Arg Leu Gln
      100      105      110
Asn Lys Glu Lys Gly Ile Met Lys Thr Met Asn Leu Asn Glu Phe Phe
      115      120      125
Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys Phe Lys Asp Thr
      130      135      140
Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu Lys Leu Ile Leu
      145      150      155      160
Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile Ser Asn Glu Asn
      165      170      175

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619

```

Met Gly Cys Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu
1      5      10      15
Glu Gln Lys Ser Asp Asp Leu Asp Cys Val Trp Thr Lys Asn Thr Ala
      20      25      30
Pro Phe Asp Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln
      35      40      45
Lys Lys Leu Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val
      50      55      60
Asp Ala Leu Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg
      65      70      75      80
Asp Phe Glu Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln
      85      90      95
Thr Leu Glu Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu
      100      105      110
Lys Gln Thr Ile Lys Asp Ile Gly Ile Arg Arg Lys Asn Phe Arg Asn
      115      120      125
Val Ser Glu Arg Ile Arg Gly Gly Asn Gly Lys Asn Ser Asp Trp Leu
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

SUBSTITUTE SHEET (RULE 26)

514

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620

```

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1             5             10             15
Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
      20             25             30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
      35             40             45
Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
      50             55             60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65             70             75             80
Val Trp Arg Ile Gln Ala Gly Lys Gly Leu
      85             90

```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621

```

Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn
 1             5             10             15
Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile
      20             25             30
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val
      35             40             45
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile
      50             55             60
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn
65             70             75             80
Met Asp Ser Pro Lys Gln Glu Asp Lys Leu Asp Lys Val Val Asp Asn
      85             90             95
Ile Lys Lys Gln Glu Ser Glu Asn Ser Met Pro Ile Gln Thr Asp Gln
      100            105            110
Ala Gln Met Glu Met Lys Thr Thr Glu Glu Lys Gln Glu Ser Gln Lys

```

SUBSTITUTE SHEET (RULE 26)

515

```

      115              120              125
Glu Leu Lys Ala Val Glu Pro Ile Pro Met Ser Thr Gln Lys Glu Ser
 130              135              140
Gln Ala Val Ala Lys Lys Glu Thr Pro His Lys Lys Pro Lys Val Ala
 145              150              155              160
Pro Lys Asp Lys Glu Ala His Lys Asp Lys Ala Lys His Ala Ala Lys
 165              170              175
Glu Pro Lys Val Lys Lys Glu Ala Arg Lys Glu Val Ser Lys Lys Ala
 180              185              190
Asn Ser Lys Thr Asn Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val
 195              200              205
Phe Ala His Thr Pro Asn Lys Ala Phe Leu Gln Glu Phe Asn Gln Phe
 210              215              220
Pro His Lys Ile Glu Asp Arg Gly Ala Thr Lys Arg Tyr Leu Ile Gly
 225              230              235              240
Pro Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser
 245              250              255
Lys Lys Met Thr Lys Pro Val Val Ile Glu Val Arg
      260              265

```

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622

```

Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe Val Leu Met
 1              5              10              15
Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys Ala Lys His
 20              25              30
Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu Glu Ser Leu
 35              40              45
Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg Gln Met Val
 50              55              60
Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu Leu Leu Asp
 65              70              75              80
Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu Phe Phe Asp
 85              90              95
Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val Leu Val Asn
 100              105              110
Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His Val Val Met
 115              120              125
Leu Lys Asp Lys Lys Leu Phe Leu Gln Ala Ser Thr Pro Ile Ala Met
 130              135              140
Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu Unk Ala Ile
 145              150              155              160
Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
      165              170

```

SUBSTITUTE SHEET (RULE 26)

516

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623

```

Met Met Ala His Ser Leu Ile Leu Val Ser Lys Thr Ser Leu Ser Asn
1           5           10           15
Leu Leu Ile Phe Val Val Gln Pro Asp Gly Lys Leu Ser Met Thr Asp
          20           25           30
Ala Ala Ile Asp Pro Asn Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg
          35           40           45
Val Asn Glu Ile Ala Glu Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu
          50           55           60
Val Thr Val Ile Asn Lys Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn
          65           70           75           80
Tyr Asn Ile Lys Asn Tyr Gly Glu Leu Glu Arg Val Ile Lys Lys Leu
          85           90           95
Pro Leu Val Arg Asp Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1           5           10           15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
          20           25           30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
          35           40           45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
          50           55           60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp

```

SUBSTITUTE SHEET (RULE 26)

517

```

65          70          75          80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
      85          90          95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
      100          105          110
His Phe Cys Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1          5          10          15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
      20          25          30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
      35          40          45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
      50          55          60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
      65          70          75          80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
      85          90          95
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg
      100          105          110
His Phe Cys Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

SUBSTITUTE SHEET (RULE 26)

518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625

```

Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu Asn
1      5      10      15
Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile Pro
20      25      30
Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser Ser
35      40      45
Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr Ile
50      55      60
Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu Ser
65      70      75      80
Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln Thr
85      90      95
Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn Ala
100     105     110
Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile Gly
115     120     125
Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met Met
130     135     140
Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala Leu
145     150     155     160
His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser His
165     170     175
Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala Leu
180     185     190
Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val Ser
195     200     205
Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp Leu
210     215     220
Tyr Tyr His Tyr Leu Lys Ile Val Lys Arg His Phe Val
225     230     235

```

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

```

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1      5      10      15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
20      25      30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
35      40      45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
50      55      60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65      70      75      80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr

```

SUBSTITUTE SHEET (RULE 26)

519

```

      85              90              95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
      100              105              110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu
      115              120              125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln
      130              135              140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile
      145              150              155              160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile
      165              170              175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile
      180              185              190
Ile Leu Lys Ala Cys Ala
      195

```

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

```

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1      5      10      15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
      20      25      30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
      35      40      45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
      50      55      60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65      70      75      80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr
      85      90      95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
      100      105      110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu
      115      120      125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln
      130      135      140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile
      145      150      155              160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile
      165              170              175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile
      180              185              190
Ile Leu Lys Ala Cys Ala
      195

```

SUBSTITUTE SHEET (RULE 26)

520

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627

```

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1           5           10           15
Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
          20           25           30
His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
          35           40           45
Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
          50           55           60
Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65           70           75           80
His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
          85           90           95
Val Gly Ile Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
          100          105          110
Tyr Phe Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
          115          120          125
Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
          130          135          140
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145          150          155          160
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
          165          170          175
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
          180          185          190
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
          195          200          205
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
          210          215          220
Ile
225

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

521

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1           5           10          15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
      20           25           30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
      35           40           45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
      50           55           60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65           70           75           80
Ala Arg Gly His Val
                        85

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

```

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1           5           10          15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
      20           25           30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
      35           40           45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
      50           55           60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65           70           75           80
Ala Arg Gly His Val
                        85

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

522

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629

```

Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile Ile Ser Phe Phe
1      5      10      15
Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu Pro Ile Val Ser
20      25      30
Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu Ile Pro Ser Tyr
35      40      45
Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr Gly Tyr Thr Ser
50      55      60
Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln Gly Val Ile Glu
65      70      75      80
Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala Ser Asn Leu Val
85      90      95
Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser Ala Trp Ala Ser
100     105     110
Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro Ser Ser Gly Cys
115     120     125
Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile Asp Val Ser Met
130     135     140
Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln Asn Phe Thr Lys
145     150     155     160
Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu Leu Gln Ile Ile
165     170     175
Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr Ala Asp Gly Leu
180     185     190
Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys Leu Gln Asn Asn
195     200     205
Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser Val Val Lys Gly
210     215     220
Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val Asn Leu Pro Asp
225     230     235     240
Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val Ser Tyr Leu Ile
245     250     255
Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe Met Lys Leu Arg
260     265     270
Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe Glu Tyr Met Arg
275     280     285
Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val Ser Phe Ile Ala
290     295     300
Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr Ser Ile Tyr Phe
305     310     315     320
Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu Phe Trp Ala Leu
325     330     335
Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu Pro Ala Val Arg
340     345     350
Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser Leu Leu Gln Gly
355     360     365
Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe Met Gln Val Thr
370     375     380
Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro Leu Ile Ala Gly
385     390     395     400
Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys Leu Ile Val Leu
405     410     415
Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile Trp Phe Ile Asn
420     425     430
Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu Leu Phe Gly Val

```

SUBSTITUTE SHEET (RULE 26)

523

```

      435              440              445
Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro Ser Val Ala Ile
  450              455              460
Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser Thr Ile Ala Ser
465              470              475              480
Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu Thr Ile Ile Glu
      485              490              495

```

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630

```

Met Ala Phe Trp Gln Ala Ile Arg Trp Trp Ile Leu Lys Leu Pro Phe
 1              5              10              15
Met Met Gly Ala Thr Met Met Trp Ile Leu Ser Glu Met Ala Phe Lys
 20              25              30
Ile Ala Gly Unk Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro
 35              40              45
Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu
 50              55              60
Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile
 65              70              75              80
Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val
 85              90              95
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr
100              105              110
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val
115              120              125
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
130              135              140

```

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

524

(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631

```

Met Gln Asn Leu Pro Gly Met Ala Arg Ala Ala Met Leu Thr Thr Ser
1      5      10      15
Ser Ala Pro Ala Pro Glu Gly Glu Gly Ala Phe Arg Ala Met Lys Met
20      25      30
Ala Ser Glu Met Ala Lys Val Glu Val Gly Tyr Val Asn Ala His Gly
35      40      45
Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile Ala Leu Lys Asn
50      55      60
Val Leu Ala Leu Lys Lys Lys Ser Leu Leu Leu Ala Pro Leu Lys Gly
65      70      75      80
Arg Leu Gly Leu Leu Gly Cys Cys Gly Val Arg Ser Arg Tyr Ser Ile
85      90      95
Met Ala Met Unk Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Thr
100     105     110
Pro Asp Pro Glu Cys Unk Leu Asp Tyr Ile Pro Asn Thr Ala Arg Glu
115     120     125
Lys Gln Val Asn Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr
130     135     140
Asn Gly Val Val Ile Phe Lys Lys Ala
145     150

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

```

Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1      5      10      15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
20      25      30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
35      40      45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
50      55      60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65      70      75      80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
85      90      95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
100     105     110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
115     120     125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
130     135     140
Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro

```

SUBSTITUTE SHEET (RULE 26)

525

```

145          150          155          160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
165          170          175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
180          185          190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
195          200          205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
210          215          220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225          230          235
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
245          250          255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
260          265          270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
275          280          285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
290          295          300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305          310          315
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
325          330          335
Phe Tyr Asp Phe Leu Val Phe
340

```

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

```

Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1          5          10          15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
20          25          30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
35          40          45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
50          55          60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65          70          75          80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
85          90          95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
100          105          110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
115          120          125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
130          135          140

```

SUBSTITUTE SHEET (RULE 26)

526

```

Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro
145          150          155          160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
          165          170          175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
          180          185          190
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
          195          200          205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
          210          215          220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225          230          235          240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
          245          250          255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
          260          265          270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
          275          280          285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
290          295          300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305          310          315          320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
          325          330          335
Phe Tyr Asp Phe Leu Val Phe
          340

```

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633

```

Met Ile Leu Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu
1          5          10          15
Ile Phe Ile Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn
          20          25          30
Glu Val Ala Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe
          35          40          45
Pro Asn Tyr Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp
          50          55          60
Ala Lys Ser Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn
65          70          75          80
Leu Ser Tyr Val Asn Asp Phe Ile Ser Lys Val Gln Lys
          85          90

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

527

(A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

```

Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1      5      10      15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
      20      25      30
Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
      35      40      45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
      50      55      60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
65      70      75      80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
      85      90      95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
      100     105     110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
      115     120     125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
      130     135     140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
145     150     155     160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
      165     170     175

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

```

Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1      5      10      15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
      20      25      30

```

SUBSTITUTE SHEET (RULE 26)

528

```

Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
   35           40           45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
   50           55           60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
   65           70           75           80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
           85           90           95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
           100          105          110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
           115          120          125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
           130          135          140
His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln
           145          150          155          160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk
           165          170          175

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635

```

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
1           5           10           15
Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
           20           25           30
Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
           35           40           45
Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
           50           55           60
Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
           65           70           75           80
Lys Leu Ile Pro Lys Ile Ile Gly
           85

```

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

529

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636

```

Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1      5      10      15
Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
      20      25      30
Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
      35      40      45
Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
      50      55      60
Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
      65      70      75      80
Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
      85      90      95
Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
      100      105      110
Gly Ala Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1      5      10      15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
      20      25      30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
      35      40      45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
      50      55      60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
      65      70      75      80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
      85      90      95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
      100      105      110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
      115      120      125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
      130      135      140

```

SUBSTITUTE SHEET (RULE 26)

530

```

Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145      150      155
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
      165      170      175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
      180      185      190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
      195      200      205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr
      210      215      220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
      225      230      235      240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
      245      250      255
Ala Lys Lys Asn
      260

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1      5      10      15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
      20      25      30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
      35      40      45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
      50      55      60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
      65      70      75      80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
      85      90      95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
      100      105      110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
      115      120      125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
      130      135      140
Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
      145      150      155      160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
      165      170      175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
      180      185      190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
      195      200      205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr

```

SUBSTITUTE SHEET (RULE 26)

531

```

      210              215              220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
225              230              235              240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
      245              250              255
Ala Lys Lys Asn
      260

```

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638

```

Met Lys Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val
1              5              10              15
Ala Asp Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro
      20              25              30
Arg Glu Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile
      35              40              45
Ile Arg Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe
      50              55              60
Gly Ser Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp
      65              70              75              80
Pro Lys Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu
      85              90              95
Leu Arg Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp
      100             105             110
Ile Gly Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala
      115             120             125
Lys Asn Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe
      130             135             140
Ile Ile Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu
      145             150             155             160
Glu Met Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile
      165             170             175
Thr Gln Asp Tyr Ala Met Ile Arg Asn Thr Ile Ala Met Met Ile
      180             185             190

```

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

532

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639

```

Met Ile Ser Glu Ile Ile Lys Phe Gln Leu Lys Gly Ile Lys Met Ile
1           5           10           15
Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys Thr Ser Leu Leu Ala Gly
20           25           30
Val Leu Leu Gly Ala Thr Ala Pro Leu Met Ala Lys Pro Leu Leu Ser
35           40           45
Asp Glu Asp Leu Leu Lys Arg Val Lys Leu His Asn Ile Lys Glu Asp
50           55           60
Thr Leu Thr Ser Cys Asn Ala Lys Val Asp Gly Ser Gln Tyr Leu Asn
65           70           75           80
Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro Gln Glu Tyr Arg Glu Lys
85           90           95
Ile Phe Glu Cys Val Glu Glu Glu Lys His Lys Gln Ala Leu Asn Leu
100          105          110
Ile Asn Lys Glu Asp Thr Glu Asp Lys Glu Glu Leu Ala Lys Lys Ile
115          120          125
Lys Glu Ile Lys Glu Lys Ala Lys Val Leu Arg Gln Lys Phe Met Ala
130          135          140
Phe Glu Met Lys Glu His Ser Lys Glu Phe Pro Asn Lys Lys Gln Leu
145          150          155          160
Gln Thr Met Leu Glu Asn Ala Phe Asp Asn Gly Ala Glu Ser Phe Ile
165          170          175
Asp Asp Trp His Glu Arg Phe Gly Gly Ile Ser Arg Glu Asn Thr Tyr
180          185          190
Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp Glu Gly Lys Ile Leu Ala
195          200          205
Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr Lys Lys Asp Phe Glu Glu
210          215          220
Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser Ala Met Ala Asn Met Ser
225          230          235          240
Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu Lys Pro Lys Tyr Gln Leu
245          250          255
His Ser Ser Asn Asn Ile Lys Pro Leu Met Ser Asn Thr Glu Leu Leu
260          265          270
Asn Met Ile Glu Leu Thr Asn Ile Lys Lys Glu Tyr Val Met Gly Cys
275          280          285
Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro Ile His Lys Asp Trp Gly
290          295          300
Phe Phe Gly Lys Ala Lys Val Pro Glu Thr Trp Arg Asn Lys Ile Trp
305          310          315          320
Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr Asp Asn Thr Thr Ala Glu
325          330          335
Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr Ser Ile Ser His His
340          345          350

```

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

533

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640

```

Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu Val
1      5      10      15
Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile Ile
20      25      30
Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg Val
35      40      45
Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met Ala
50      55      60
Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val Glu
65      70      75      80
Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu Met
85      90      95
Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro Met
100     105     110
Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro Met
115     120     125
Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn Arg
130     135     140
Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg Gln
145     150     155     160
Val Met Gln Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met Tyr
165     170     175
Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile Val
180     185     190
Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile Gly
195     200     205
His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile Glu
210     215     220
Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu Thr
225     230     235     240
Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser Gly
245     250     255
Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser Leu
260     265     270
Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn Lys
275     280     285
Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg Tyr
290     295     300
Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile Lys
305     310     315     320
Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu Met
325     330     335
Leu Glu Glu Gln Arg Arg Gln Ser Trp Ala Met Leu Trp Ser
340     345     350

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

534

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```

Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1           5           10           15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
          20           25           30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
          35           40           45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
          50           55           60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
65          70           75           80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
          85           90           95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
          100          105          110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
          115          120          125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
130          135          140
Gly
145

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

```

Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1           5           10           15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
          20           25           30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
          35           40           45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
          50           55           60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
65          70           75           80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro

```

SUBSTITUTE SHEET (RULE 26)

535

```

      85              90              95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
      100              105              110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
      115              120              125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile
      130              135              140
Gly
145

```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642

```

Met Pro Thr Met Leu Ala Val Gly Phe Trp Val Leu Val Phe Leu Ser
1      5      10      15
Thr Ser Asn Ala Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser
      20      25      30
Val Pro Ser Ile Phe Thr Leu Leu Ser Leu Ser Ile Phe Val Tyr Val
      35      40      45
Ala Gly Asn Ala Glu Phe Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile
      50      55      60
Asp Val Gly Glu Leu Phe Val Ile Ser Leu Ala Leu Val Gly Ser Leu
      65      70      75      80
Phe Gly Phe Leu Trp Tyr Asn Cys Asn Pro Ala Ser Val Phe Met Gly
      85      90      95
Asp Ser Gly Ser Leu Ala Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile
      100     105     110
Val Ser His Asn Glu Ile Leu Leu Val Leu Met Gly Ser Ile Phe Val
      115     120     125
Ile Glu Thr Leu Ser Val Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg
      130     135     140
Lys Lys Arg Leu Phe Leu Met Ala Pro Ile His His Phe Glu Gln
145     150     155     160
Lys Gly Trp Ala Glu Asn Lys Val Ile Val Arg Phe Trp Ile Ile Ser
      165     170     175
Met Leu Ser Asn Leu Val Ala Leu Leu Ser Leu Lys Val Cys
      180     185     190

```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

536

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643

```

Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala Thr
1      5      10      15
Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu Ser
20     25     30
Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe Phe
35     40     45
Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu Lys
50     55     60
Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn Leu
65     70     75     80
Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser Leu
85     90     95
Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser Asp
100    105    110
Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp Asn
115    120    125
Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys Thr
130    135    140
Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly Phe
145    150    155    160
Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Ser Asp Leu Ile Thr
165    170    175
Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr Gly
180    185    190
Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys Glu
195    200    205
Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys Ala
210    215    220
Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr Phe
225    230    235    240
His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu Asn
245    250    255
Ser Asp Ala Unk Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu Asn
260    265    270
Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu Glu
275    280    285
Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu Lys
290    295    300
Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp Phe
305    310    315    320
Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile Glu
325    330    335
Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu Asn
340    345    350
Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr Glu
355    360    365
Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn Leu
370    375    380
Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser Ile
385    390    395    400
Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser Thr
405    410    415
Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Ala

```

SUBSTITUTE SHEET (RULE 26)

537

```

          420          425          430
Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu Ser
          435          440          445
Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu Ala
          450          455          460
Ile Lys Glu Gln Ala Glu Thr Lys Arg Cys Asn Ala Gly Asn Ala Phe
465          470          475          480
Cys Asp Thr Tyr Gln Pro Cys Lys Pro
          485

```

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1          5          10          15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
          20          25          30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
          35          40          45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
          50          55          60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65          70          75          80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
          85          90          95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
          100          105          110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
          115          120          125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
          130          135          140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145          150          155          160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
          165          170          175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
          180          185          190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
          195          200          205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
          210          215          220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225          230          235          240
Val Phe Leu Ser Gly Val Lys Asn
          245

```

SUBSTITUTE SHEET (RULE 26)

538

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1           5           10           15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
          20           25           30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
          35           40           45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
          50           55           60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
          65           70           75           80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
          85           90           95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
          100          105          110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
          115          120          125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
          130          135          140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
          145          150          155          160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
          165          170          175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
          180          185          190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
          195          200          205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
          210          215          220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
          225          230          235          240
Val Phe Leu Ser Gly Val Lys Asn
          245

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

539

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
 1           5           10           15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
 20           25           30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
 35           40           45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
 50           55           60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
 65           70           75           80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
 85           90           95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
 100          105          110
Leu Leu Trp Trp Phe Unk Leu
 115

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
 1           5           10           15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
 20           25           30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
 35           40           45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
 50           55           60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
 65           70           75           80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
 85           90           95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
 100          105          110
Leu Leu Trp Trp Phe Unk Leu
 115

```

SUBSTITUTE SHEET (RULE 26)

540

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

```

Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1      5      10      15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
      20      25      30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
      35      40      45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
      50      55      60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser
      65      70      75      80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
      85      90      95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
      100      105

```

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

```

Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1      5      10      15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
      20      25      30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
      35      40      45
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
      50      55      60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser

```

SUBSTITUTE SHEET (RULE 26)

541

```

65          70          75          80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
          85          90          95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
          100          105

```

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647

```

Val Phe Lys Asn Ser Leu Phe Gly Ile Ser Ile Ser Met Leu Ile Thr
1          5          10          15
Trp Val Leu Thr Ala Cys Ile Leu Ile Phe Ile Leu Phe Val Pro Asn
          20          25          30
Phe Thr Leu Thr His Pro Asn Phe His Phe Thr Pro Phe Glu Lys Thr
          35          40          45
Tyr Phe Gln Ile Leu Gly Leu Val Gly Ile Val Ser Ser Ile Ile Phe
          50          55          60
Thr Gly Phe Leu Ala Asp Lys Ile Lys Pro His Lys Val Cys Met Ala
65          70          75          80
Phe Ser Thr Thr Phe Gly Phe Phe Gly Phe Leu Phe Phe Lys Glu Phe
          85          90          95
Tyr Ser Asn Ala Pro Ser Leu Val Asn Thr Ile Ile Leu Tyr Phe Leu
          100          105          110
Ala Cys Phe Cys Ala Gly Ile Met Asn Phe Cys Pro Ile Phe Met Ser
          115          120          125
Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr
          130          135          140
Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser
145          150          155          160
Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr
          165          170          175
Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr
          180          185          190
Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu
          195          200          205
Val Ser Pro Thr Ala
210

```

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

542

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```

Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1      5      10      15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
      20      25      30
Leu Val Leu Ala Ser Ile Trp Val Phe Leu Ala Leu Gly Val Leu
      35      40      45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
50      55      60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65      70      75      80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
      85      90      95
Tyr Leu Gln Glu Lys Unk Unk Ile Phe Pro Thr Unk Lys Unk Unk
      100     105     110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
      115     120     125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
130     135     140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
145     150     155

```

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

```

Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1      5      10      15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
      20      25      30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
      35      40      45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
50      55      60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65      70      75      80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala

```

SUBSTITUTE SHEET (RULE 26)

543

				85				90					95			
Tyr	Leu	Gln	Glu	Lys	Unk	Unk	Ile	Phe	Pro	Thr	Unk	Lys	Unk	Unk	Unk	Unk
			100					105					110			
Ser	Lys	Ile	Met	Arg	Leu	Asp	Gly	Val	Lys	His	Val	Glu	Lys	Asn	Leu	
		115					120					125				
Lys	Asp	Asn	Leu	Glu	Glu	Met	Ser	Asp	Glu	Val	Lys	Asn	Lys	Gly	Ser	
		130				135					140					
Ile	Asp	Asn	Ala	Lys	Glu	Ser	Phe	Asn	Lys	Gly	Tyr	Gly				
145					150					155						

(2) INFORMATION FOR SEO ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649

Met	Lys	Ser	Asp	Lys	Pro	Phe	Leu	Glu	Arg	Tyr	Phe	Tyr	Asp	Pro	Thr
1			5						10				15		
Leu	Leu	Gln	Lys	Gly	Leu	Ile	Phe	Ala	Leu	Tyr	Pro	Phe	Ser	Leu	Ile
			20					25					30		
Tyr	Gln	Cys	Ile	Ala	Thr	Ile	Lys	Arg	Lys	Thr	Ala	Lys	Lys	His	Asp
		35					40					45			
Phe	Lys	Ile	Pro	Ile	Ile	Ser	Ile	Gly	Asn	Leu	Ile	Ala	Gly	Gly	Ser
	50					55					60				
Gly	Lys	Thr	Pro	Phe	Ile	Leu	Glu	Ile	Ala	Pro	Arg	Tyr	Gln	Glu	Val
65				70						75					80
Ala	Val	Val	Ser	Arg	Gly	Tyr	Gln	Arg	Asp	Ser	Lys	Gly	Leu	Val	Val
				85					90					95	
Val	Ser	Val	Lys	Gly	Asn	Ile	Leu	Val	Pro	Gln	Lys	Thr	Ala	Gly	Asp
			100					105					110		
Glu	Ala	Tyr	Leu	Leu	Ala	Leu	Asn	Leu	Lys	Gln	Ala	Ser	Val	Ile	Val
		115					120					125			
Ser	Glu	Lys	Arg	Glu	Leu	Gly	Val	Leu	Lys	Ala	Leu	Glu	Leu	Gly	Ser
	130					135					140				
Lys	Ile	Val	Phe	Leu	Asp	Asp	Gly	Phe	Arg	Phe	Asn	Phe	Asn	Gln	Phe
145				150						155					160
Asn	Ala	Leu	Leu	Lys	Pro	Lys	Val	Pro	Pro	Tyr	Tyr	Pro	Phe	Cys	Leu
				165					170					175	
Pro	Ser	Gly	Leu	Tyr	Arg	Glu	Asn	Ile	Lys	Ser	Tyr	Lys	Glu	Ala	His
			180					185					190		
Leu	Val	Ile	Thr	Glu	Asp	Lys	Asp	Tyr	Gln	Arg	Ile	Thr	Ser	Ile	Thr
		195					200					205			
Asn	Pro	Thr	Lys	Arg	Met	Leu	Leu	Val	Thr	Ala	Ile	Ala	Asn	Pro	Ser
						215					220				
Arg	Leu	Asp	Ala	Phe	Leu	Pro	Lys	Glu	Val	Val	Lys	Lys	Leu	Tyr	Phe
225				230						235					240
Arg	Asp	His	Ala	Pro	Phe	Asp	Leu	Lys	Leu	Leu	Glu	Lys	Glu	Phe	Tyr
				245					250					255	
Gln	Asn	Asn	Ala	Thr	Ser	Leu	Leu	Val	Thr	Ser	Lys	Asp	Leu	Val	Lys
			260					265					270		

SUBSTITUTE SHEET (RULE 26)

544

Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
 275 280 285
 Ile Cys Pro Lys Val Leu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
 290 295 300
 Pro Cys Asn Ile Lys Glu His Leu
 305 310

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...56

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650

Met Ser Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu
 1 5 10 15
 Gly Val Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro
 20 25 30
 Asn Asn Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser
 35 40 45
 Ser Thr Ser Lys Phe Ile Leu Leu
 50 55

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651

Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys Ile
 1 5 10 15
 Gly Ala Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asn Glu Ile Ser
 20 25 30
 Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala Pro
 35 40 45
 Asp Val Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile Cys

SUBSTITUTE SHEET (RULE 26)

545

```

      50              55              60
Asp Lys Gly Glu Trp Val Glu Val Gly Gly Ala Ala Asn Ala Ser Lys
65              70              75              80
Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe Leu
      85              90              95
Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala Gly
      100              105              110
Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val Asn
      115              120              125
Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser Ser
      130              135              140
Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His Gly
145              150              155              160
Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser His
      165              170              175
Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp
      180              185              190
Tyr Ala Gly Arg Leu Leu Glu
      195

```

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

```

Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1              5              10              15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
      20              25              30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
      35              40              45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
50              55              60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Unk Arg Thr Met Arg
65              70              75              80
Ala

```

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

546

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

```

Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1          5          10          15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
          20          25          30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
          35          40          45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
          50          55          60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Unk Arg Thr Met Arg
65          70          75          80
Ala

```

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653

```

Met Leu Lys Asn Gly Asp Lys Ile Pro Asp Ala Ile Leu Val Asp Ile
1          5          10          15
Glu Met Pro Lys Met Asp Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys
          20          25          30
Tyr Asn Lys Phe Lys Asn Leu Pro Leu Ile Ala Val Thr Ser Arg Val
          35          40          45
Thr Lys Thr Asp Arg Met Arg Gly Val Glu Ser Gly Met Thr Glu Tyr
          50          55          60
Ile Thr Lys Pro Tyr Ser Gly Glu Tyr Leu Thr Thr Val Val Lys Arg
65          70          75          80
Ser Ile Lys Leu Glu Gly Asp Gln Ser
          85

```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

547

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...111
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654

```

Val Phe Glu Pro Val Ile Ala Tyr Lys Leu Phe His Ser Phe Val Ile
1          5          10          15
Leu Gly Cys Ala Ile Glu Thr Leu Thr Thr Lys Cys Val Glu Gly Ile
          20          25          30
Thr Ala Asn Glu Lys Ile Cys His Asp Tyr Val Phe Asn Ser Ile Gly
          35          40          45
Ile Val Thr Ala Leu Asn Pro His Ile Gly Tyr Glu Lys Ser Ala Met
          50          55          60
Ile Ala Lys Glu Ala Leu Lys Ser Asp Arg Ser Ile Tyr Asp Ile Ala
65          70          75          80
Leu Glu Lys Lys Ile Leu Thr Lys Glu Gln Leu Asp Asp Ile Phe Lys
          85          90          95
Pro Glu Asn Met Leu Arg Thr His Ala Phe Lys Lys His Lys Asp
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655

```

Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1          5          10          15
Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
          20          25          30
Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
          35          40          45
Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
50          55          60
Gln
65

```

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 amino acids

SUBSTITUTE SHEET (RULE 26)

548

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656

```

Met Lys Lys Leu Leu Leu Leu Glu His Lys Ile Val Lys Ile Gly
 1          5          10          15
Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu Phe Tyr Glu Gln
          20          25          30
Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly Lys Phe Pro Thr
          35          40          45
Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys Asn Lys Ile Asp
 50          55          60
Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys Ser Val Asn Glu
 65          70          75          80
Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe Asn Ala Leu Val
          85          90          95
Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys Thr Leu Ile Lys
          100          105          110
Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn Glu Asp Glu Lys
          115          120          125
Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser Gln Lys Glu Thr
          130          135          140
Gln Pro Pro Ile Ser Ile Lys Asn Ser Val Ser His Ile Lys Ser Lys
          145          150          155          160
Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro Ser Val Ser Phe
          165          170          175
Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Phe Ser Ser Phe Glu
          180          185          190
Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys Glu Lys Leu Lys
          195          200          205
Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser Leu Leu Ser Ser
          210          215          220
Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu Ile Gly Leu Ile
          225          230          235          240
Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn Ala Ser Asn Asn
          245          250          255
Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
          260          265

```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657

```

Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser
1           5           10           15
Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu
          20           25           30
Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys
          35           40           45
Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu
          50           55           60
Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys
65           70           75           80
Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn
          85           90           95
Leu Lys Gln Gly
          100

```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658

```

Val Met Asp Lys Leu Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala
1           5           10           15
Tyr Leu Gly Lys Ile Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn
          20           25           30
Glu His Pro Gln Thr Ile Ala Leu Ile Leu Ala His Met Glu Unk Pro
          35           40           45
Asn Ala Ala Glu Thr Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu
          50           55           60
Ile Ser Ile Arg Met Ala Asn Phe Arg Arg Asn Ile Ala Pro Ser Gly
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

550

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659

```

Met Arg Tyr Phe Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe
1          5          10          15
Phe Val Ser Cys Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr
20          25          30
Lys Glu Arg Ile Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr
35          40          45
Leu Asn Ala Leu Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val
50          55          60
Phe Arg Phe Tyr Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn
65          70          75          80
Thr Glu Val Thr Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr
85          90          95
Met Thr Lys Arg Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp
100         105         110
Ile Ala Ala Arg Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe
115         120         125
Asp Asp Ile Val Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg
130         135         140
His Leu Thr Pro Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu
145         150         155         160
Ile Ile Leu Tyr Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu
165         170         175
Thr Gln Lys Ile Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln
180         185         190
Asp Leu Glu Asp Asn Glu Asn Ala Asp Ser Glu Leu Gln
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660

```

Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
1          5          10          15
Val Val Glu Pro Val Ala Arg Ile Gly Ile Unk Ala Phe Thr Asn Asp
20          25          30
Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
35          40          45
Thr Ile Asn Gly Glu Asn Arg Pro Leu Unk Gly Asn Pro Ile Leu Gly

```

SUBSTITUTE SHEET (RULE 26)

551

```

      50              55              60
Trp Asp Glu Glu Gly Lys Leu Lys Phe Gly Lys Ile Arg His Lys Tyr
65              70              75              80
Leu Glu Thr Ser Asn Val Asn Ala Gly Asn Ala Leu Thr Asn Leu Ile
      85              90              95
Leu Met Gln Arg Gly Tyr Ser Met Asn Ala Arg Ala Phe Gly Ala Gly
      100              105              110
Asp Asp Met Ile Lys Glu Ala Ile Ser Leu Lys Lys
      115              120

```

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661

```

Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His
1              5              10              15
Val Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala
      20              25              30
Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr
      35              40              45
Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val
      50              55              60
Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala
65              70              75              80
Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
      85              90

```

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

SUBSTITUTE SHEET (RULE 26)

552

```

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1      5      10      15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
      20      25      30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
      35      40      45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
      50      55      60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65      70      75      80

```

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

```

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1      5      10      15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
      20      25      30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
      35      40      45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
      50      55      60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Pro Met Gln Unk
65      70      75      80

```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663

```

Val Glu Glu Leu Ala Lys Leu Ile Asn Asn Asn Asn Asn Asn Lys Lys

```

SUBSTITUTE SHEET (RULE 26)

553

```

1           5           10           15
Leu Arg Gly Phe Phe Leu Lys Val Leu Leu Ser Leu Val Val Phe Ser
                20           25           30
Ser Tyr Gly Ser Ala Asn Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu
                35           40           45
Glu Lys Glu Lys Asn Thr Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp
                50           55           60
Phe Asp Ser Phe Lys Ala Thr Ile Lys Asn Leu Lys Asp Lys Lys Val
                65           70           75           80
Thr Phe Lys Glu Val Asn Pro Asp Ile Ile Lys Asp Glu Val Phe Asp
                85           90           95
Phe Val Ile Val Asn Arg Val Leu Lys Lys Ile Lys Asp Leu Lys His
                100           105           110
Tyr Asp Pro Val Ile Glu Lys Ile Phe Asp Glu Lys Gly Lys Glu Met
                115           120           125
Gly Leu Asn Val Glu Leu Gln Ile Asn Pro Glu Val Lys Asp Phe Phe
                130           135           140
Thr Phe Lys Ser Ile Ser Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser
                145           150           155           160
Leu His Gly Glu Thr Arg Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn
                165           170           175
Val Leu Leu Ala Val Phe Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys
                180           185           190
His Ile Ser Thr Ile Glu Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr
                195           200           205
Cys Glu Ala Val Tyr Leu
                210

```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664

```

Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser Thr Tyr Met Val
1           5           10           15
Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser Ala Leu Asp Leu
                20           25           30
Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys Ala Tyr Pro Lys
                35           40           45
Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu Asn Gly Ser Leu
                50           55           60
Glu Pro Thr Asn Glu Gly Tyr Ala Leu Pro Asn Ser Leu Unk
                65           70           75

```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

SUBSTITUTE SHEET (RULE 26)

554

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665

```

Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe Asn Val Ile Ile
1      5      10      15
Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile His Lys Thr Leu
20      25      30
Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly Lys Leu Gly Ile
35      40      45
Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser Leu Glu Val Glu
50      55      60
Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro Thr Lys Lys Arg
65      70      75      80
Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr Gly Ile Trp Ala
85      90      95
Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile Ile Leu Asp Asp
100     105     110
Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys Tyr Glu Unk Arg
115     120     125
Ile Ser Arg Asn Gln Arg Gly Ile Phe Pro Arg Arg Arg Leu Lys Ile
130     135     140
Ser Ser Leu Lys Ser Ser Ile Cys Phe Leu Lys Met Leu Lys Ser Lys
145     150     155     160
Trp Met Ala Thr Pro Thr Ile Unk Pro Lys Pro Gly Lys Trp Arg Ser
165     170     175
Ile

```

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666

```

Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1      5      10      15
Trp Gly Arg Cys Val Tyr Ala Gly Gly Leu Met Ala Glu Gln Asp Pro

```

SUBSTITUTE SHEET (RULE 26)

555

```

      20      25      30
Lys Glu Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn Phe
  35      40      45
Thr Arg Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp Ala
  50      55      60
Asp Gly Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala Ile
  65      70      75      80
Ala Arg Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His Thr
      85      90      95
Ala Thr Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys Asp
  100      105      110
Leu Ala Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu Glu
  115      120      125
Tyr Tyr Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met Leu
  130      135      140
Ser Ala Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp Lys
  145      150      155      160
Lys Asp Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Gly
      165      170      175
Gly Cys Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val Thr
      180      185      190
Lys Asp Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu Leu
  195      200      205
Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu Gly
  210      215      220
Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu Lys
  225      230      235      240
Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu Gln
      245      250      255
Lys Gln

```

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667

```

Val Ala Leu Thr Leu Gly Ala Arg Gly Gly Val Tyr Leu Cys Gly Gly
1      5      10      15
Ile Ile Pro Arg Phe Ile Asp Tyr Phe Lys Thr Ser Pro Phe Arg Ala
  20      25      30
Arg Phe Glu Thr Lys Gly Arg Met Gly Ala Phe Leu Ala Ser Ile Pro
  35      40      45
Val His Val Val Met Lys Lys Thr Pro Gly Leu Asp Gly Ala Gly Ile
  50      55      60
Ala Leu Glu Asn Tyr Leu Leu His Asp Arg Ile
  65      70      75

```

SUBSTITUTE SHEET (RULE 26)

556

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668

```

Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
1      5      10      15
Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
20      25      30
Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
35      40      45
Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
50      55      60
Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
65      70      75      80
Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
85      90      95
Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
100     105     110
Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
115     120     125
Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
130     135     140
Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
145     150     155     160
Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
165     170     175
Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
180     185     190
Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
195     200     205
Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
210     215     220
Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Lys Val Asn Asp
225     230     235     240
Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
245     250     255
Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
260     265     270
Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
275     280     285
Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
290     295     300
Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Ile Lys Ala Ser Asn
305     310     315     320
Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
325     330     335
Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
340     345     350
Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr

```

SUBSTITUTE SHEET (RULE 26)

557

```

      355              360              365
Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
      370              375              380
Glu Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
      385              390              395              400
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
      405              410              415
Phe Ser Ile Trp Asp
      420

```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669

```

Met Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala
1              5              10              15
Val Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu
      20              25              30
Val Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys
      35              40              45
Ala Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val
      50              55              60
Asn Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe
      65              70              75              80
Ile

```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670

SUBSTITUTE SHEET (RULE 26)

558

```

Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr Phe
1      5      10      15
Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu Ile
20      25      30
Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met Ser
35      40      45
Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr Ser
50      55      60
Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu Arg
65      70      75      80
Pro Lys Arg Phe Gly Phe Lys Ile Ala Phe Phe Asp Arg Ser Arg His
85      90      95
Gln His Val Phe Ile Leu Pro His Arg Ala Lys Asp Phe Lys Lys Ala
100      105      110

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

```

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1      5      10      15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
20      25      30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
35      40      45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
50      55      60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65      70      75      80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
85      90      95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
100      105      110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
115      120      125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
130      135      140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145      150      155      160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
165      170      175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
180      185      190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
195      200      205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
210      215      220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr

```

SUBSTITUTE SHEET (RULE 26)

559

```

225          230          235          240
Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
          245          250          255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
          260          265          270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
          275          280          285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
          290          295          300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305          310          315          320
Thr Phe Thr Phe Asn
          325

```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

```

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp
1          5          10          15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
          20          25          30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
          35          40          45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
          50          55          60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65          70          75          80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
          85          90          95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
          100          105          110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
          115          120          125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
          130          135          140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145          150          155          160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
          165          170          175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
          180          185          190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
          195          200          205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
210          215          220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr
225          230          235          240

```

SUBSTITUTE SHEET (RULE 26)

560

```

Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
                245                250                255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
                260                265                270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
                275                280                285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
                290                295                300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305                310                315                320
Thr Phe Thr Phe Asn
                325

```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

```

Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser
1      5      10      15
Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser
20     25     30
Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala
35     40     45
Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn
50     55     60
Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly
65     70     75     80
Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys
85     90     95
Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe
100    105    110
Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn
115    120    125
Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu
130    135    140
Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile
145    150    155    160
Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser
165    170    175
Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly
180    185    190
Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly
195    200    205
Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg
210    215    220
Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr
225    230    235    240
Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile

```

SUBSTITUTE SHEET (RULE 26)

561

Gln Thr Ala Asp Ala Met Leu Gln Thr Val Asn Ser Leu Lys Arg
 245 250 255
 260 265 270

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...271
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

Leu	Leu	Ser	Leu	Val	Lys	Gly	Lys	Thr	Met	Leu	Arg	Ser	Leu	Tyr	Ser
1				5					10					15	
Ala	Thr	Ser	Gly	Met	Leu	Ala	Gln	Gln	Thr	His	Ile	Asp	Thr	Thr	Ser
			20					25					30		
Asn	Asn	Ile	Ala	Asn	Val	Asn	Thr	Thr	Gly	Phe	Lys	Lys	Ser	Arg	Ala
		35					40					45			
Asp	Phe	Asn	Asp	Leu	Phe	Tyr	Gln	Ala	Met	Gln	Tyr	Ala	Gly	Thr	Asn
	50					55					60				
Thr	Ser	Asn	Thr	Thr	Leu	Ser	Pro	Asp	Gly	Met	Glu	Val	Gly	Leu	Gly
65					70					75				80	
Val	Arg	Pro	Ser	Ala	Ile	Thr	Lys	Met	Phe	Ser	Gln	Gly	Ser	Pro	Lys
				85					90					95	
Glu	Thr	Glu	Asn	Asn	Leu	Asp	Ile	Ala	Ile	Thr	Gly	Lys	Gly	Phe	Phe
			100					105					110		
Gln	Val	Gln	Leu	Pro	Asp	Gly	Thr	Thr	Ala	Tyr	Thr	Arg	Ser	Gly	Asn
			115				120					125			
Phe	Lys	Leu	Asp	Glu	Gln	Gly	Asn	Leu	Val	Thr	Ser	Glu	Gly	Tyr	Leu
	130					135					140				
Leu	Ile	Pro	Gln	Ile	Thr	Leu	Pro	Glu	Asp	Thr	Thr	Gln	Val	Asn	Ile
145					150					155				160	
Gly	Val	Asp	Gly	Thr	Val	Ser	Val	Thr	Gln	Gly	Leu	Gln	Thr	Thr	Ser
				165					170					175	
Asn	Val	Ile	Gly	Gln	Ile	Thr	Leu	Ala	Asn	Phe	Val	Asn	Pro	Ala	Gly
			180					185					190		
Leu	His	Ser	Met	Gly	Asp	Asn	Leu	Phe	Ser	Ile	Thr	Asn	Ala	Ser	Gly
		195					200					205			
Asp	Ala	Ile	Val	Gly	Asn	Pro	Asp	Ser	Gln	Gly	Leu	Gly	Lys	Leu	Arg
	210					215					220				
Gln	Gly	Phe	Leu	Glu	Leu	Ser	Asn	Val	Arg	Leu	Val	Glu	Glu	Met	Thr
225					230					235				240	
Asp	Leu	Ile	Thr	Ala	Gln	Arg	Ala	Tyr	Glu	Ala	Asn	Ser	Lys	Ser	Ile
				245					250					255	
Gln	Thr	Ala	Asp	Ala	Met	Leu	Gln	Thr	Val	Asn	Ser	Leu	Lys	Arg	
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids

SUBSTITUTE SHEET (RULE 26)

562

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673

```

Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser Tyr Cys Leu
1           5           10           15
Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu
           20           25           30
Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val Leu Ile Leu
           35           40           45
Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile
50           55           60
Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe Phe
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674

```

Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
1           5           10           15
Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
           20           25           30
Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
           35           40           45
Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
50           55           60
Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
65           70           75           80
Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
           85           90           95
Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
           100          105          110
Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
           115          120          125
Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu

```

SUBSTITUTE SHEET (RULE 26)

563

```

130          135          140
Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp
145          150          155          160
Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln
          165          170          175
Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu
          180          185          190
Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg
          195          200          205
Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser
          210          215          220
Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn
          225          230          235          240
Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp
          245          250          255
Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn
          260          265          270
Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser
          275          280          285
Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val
          290          295          300
Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro
          305          310          315          320
Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys
          325          330          335
Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro
          340          345          350
Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser
          355          360          365
Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp
          370          375          380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val
          385          390          395          400

```

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

```

Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe
1          5          10          15
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn
          20          25          30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr
          35          40          45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser
          50          55          60
Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

564

Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val
85 90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

```

Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe
1      5      10      15
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn
20      25      30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr
35      40      45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser
50      55      60
Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk
65      70      75      80
Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val
85      90

```

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676

```

Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro Asn Lys Gln Glu Leu
1      5      10      15
Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly Lys Ile Leu Ala Ser
20      25      30
Leu Leu Gly Gly Gly Thr Asn Leu Phe Thr Gly Leu Ser Ser Asp Leu
35      40      45
Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu Met Leu Met Met Gly

```

SUBSTITUTE SHEET (RULE 26)

565

```

      50              55              60
Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu Pro Met Asp Asn Ile
65              70              75              80
Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly Phe Asp Ser Ile Lys
      85              90              95
Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe Gly Ser Ser Lys Ser
      100             105             110
Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln Val Arg Leu
      115             120             125

```

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

```

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Unk Phe Gly Ala Gly Gly
1              5              10              15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
      20              25              30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
      35              40              45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
      50              55              60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
      65              70              75              80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Unk Thr Tyr
      85              90              95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Unk Asp Lys Thr
      100             105             110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
      115             120             125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
      130             135             140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
      145             150             155             160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
      165             170             175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Unk
      180             185             190
Gln Pro Gly
      195

```

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

566

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

```

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Unk Phe Gly Ala Gly Gly
1           5           10           15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
20           25           30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
35           40           45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
50           55           60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65           70           75           80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Unk Thr Tyr
85           90           95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Unk Asp Lys Thr
100          105          110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
115          120          125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
130          135          140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145          150          155          160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
165          170          175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Unk
180          185          190
Gln Pro Gly
195

```

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678

```

Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
1           5           10           15
Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu

```

SUBSTITUTE SHEET (RULE 26)

567

```

      20              25              30
Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
      35              40              45
Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
      50              55              60
Glu Val Ile Tyr Glu Val Ile Glu
65              70

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679

```

Met Ala Gly Leu Val Leu Met Val Leu Leu Ala Ser Tyr Glu Ser Phe
1              5              10              15
Val Ser Lys Leu Asp Lys Val Asp Ala Ser Glu Ile Thr Trp Leu Lys
      20              25              30
His Thr Asp Phe Asn Ala Leu Lys Leu Lys Val Ser Leu Ser Ile Val
      35              40              45
Ala Ile Ser Ala Ile Phe Leu Leu Lys Arg Tyr Met Ser Leu Glu Asp
      50              55              60
Val Leu Ser Ser Ile Pro Lys Asp Thr Pro Leu Ser His Asn Pro Ile
65              70              75              80
Phe Trp Gln Val Val Ile His Leu Val Phe Val Cys Ser Ala Leu Leu
      85              90              95
Thr Ala Val Thr Asn Asn Ile Ala Phe Ser Gln Lys Glu Arg His
      100              105              110

```

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680

SUBSTITUTE SHEET (RULE 26)

568

```

Met Ile Thr Ile Val Ile Ala Lys Ala Gly Asn Ile Val Lys Unk Asp
1           5           10           15
Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly Gly
20           25           30
Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala Lys
35           40           45
Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys Asp
50           55           60
Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys Thr
65           70           75           80
Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg Asp
85           90           95
Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile Leu
100          105          110
Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Unk Leu Ala Unk
115          120          125
Unk Leu Glu Thr Thr Asp Leu Tyr Tyr Ala Ser Asp Val Phe
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681

```

Val Asn Phe Asn Ala Lys Asn Ile Ser Ile Asp Asn Leu Val Glu Ile
1           5           10           15
Asn Asn Arg Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val
20           25           30
Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr Unk Ser Lys Asn Ala Glu
35           40           45
Ile Ser Leu Tyr Asp Gly Ala Thr Unk Ile Trp Leu Gln Thr Gly
50           55           60

```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

569

(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682

```

Met Arg Thr Leu Ile Leu Ser Leu Leu Lys His Ala Ile Leu Met Gly
1      5      10      15
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
20      25      30
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
35      40      45
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
50      55      60
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
65      70      75      80
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
85      90      95
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
100     105     110
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
115     120     125
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
130     135     140
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
145     150     155     160
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr
165     170     175
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
180     185     190
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
195     200     205
Thr Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
210     215     220
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
225     230     235     240
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
245     250     255
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
260     265     270
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
275     280     285
Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
290     295     300
Ile Ser Pro Tyr Asp Leu
305     310

```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...169

SUBSTITUTE SHEET (RULE 26)

570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683

```

Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys
1      5      10      15
Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala
20      25      30
Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly
35      40      45
Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln
50      55      60
Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro
65      70      75      80
Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met
85      90      95
His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu
100     105     110
Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe
115     120     125
Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly
130     135     140
Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn
145     150     155     160
Ala Cys Thr Phe Pro Lys Val Glu Phe
165

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

```

Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
1      5      10      15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
20      25      30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
35      40      45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
50      55      60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
65      70      75      80
Tyr Pro Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

571

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

```

Met Arg Unk Glu Lys Ile Met Thr Asn Phe Glu Lys Unk Ile Ala Gln
 1           5           10           15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
      20           25           30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
      35           40           45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
      50           55           60
Unk Thr Ile Val Met Phe Val Val Ala Phe Val Ile Unk Unk Ser Leu
65           70           75           80
Tyr Pro Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

```

Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
 1           5           10           15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
      20           25           30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
      35           40           45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
      50           55           60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

SUBSTITUTE SHEET (RULE 26)

572

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

```

Met Unk Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1          5          10          15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
          20          25          30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
          35          40          45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Unk Pro Val Gly
          50          55          60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

```

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1          5          10          15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
          20          25          30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
          35          40          45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
          50          55          60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65          70          75          80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
          85          90          95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
          100          105          110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
          115          120          125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly

```

SUBSTITUTE SHEET (RULE 26)

573

```

      130              135              140
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145              150              155              160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
      165              170              175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp
      180              185              190
Arg Leu Unk Unk
      195

```

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

```

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1              5              10              15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
      20              25              30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
      35              40              45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
      50              55              60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
      65              70              75              80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
      85              90              95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
      100             105             110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
      115             120             125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
      130             135             140
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
      145             150             155             160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
      165             170             175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp
      180             185             190
Arg Leu Unk Unk
      195

```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

574

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687

```

Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser Leu
1      5      10      15
Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala Asn
20     25     30
Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly Leu
35     40     45
Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe Glu
50     55     60
Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val Phe
65     70     75     80
Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys Ile
85     90     95
Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser Thr
100    105    110
Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr Phe
115    120    125
Ile Ala Phe Leu Phe Ala Ile Phe Tyr Ala Gly Gly Tyr Gln
130    135    140

```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688

```

Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile Phe
1      5      10      15
Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly Tyr
20     25     30
Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu Ser
35     40     45
Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Arg Lys Lys
50     55     60
Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys Lys
65     70     75     80
Ala Cys Glu Glu Val Phe

```

SUBSTITUTE SHEET (RULE 26)

575

85

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689

```

Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser
1          5          10          15
Gly Pro Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val
          20          25          30
Ala Lys Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn
          35          40          45
Arg Ala Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu
          50          55          60
Phe Gly Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His
          65          70          75          80
His Leu Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys
          85          90          95
Asp Tyr Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Lys Phe Thr
          100          105          110
Asp Arg Leu Asn Glu Gly Glu Ala Leu
          115          120

```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690

```

Met Thr Ile Thr Thr Leu Ser Phe Leu Phe Thr Thr Pro Glu Val Phe
1          5          10          15
Val Asn Gln Asp Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

576

Lys Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp
 35 40 45
 Arg Asn Ala Ile Trp Arg Val Lys Gly Phe Ala
 50 55

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691

Val Phe Ser Gly Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser
 1 5 10 15
 Ala Phe Val Ile Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro
 20 25 30
 Leu Gly Arg Glu Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val
 35 40 45
 Ile Gly Tyr Gly Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala
 50 55 60
 Pro Asn Ala Lys Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile
 65 70 75 80
 Asn Val Leu Ala Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu
 85 90 95
 Tyr Tyr Leu Lys Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala
 100 105 110
 Leu Gln Lys Cys Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala
 115 120 125
 Ala Asn Unk Unk Val Ala His Thr Glu Asp Unk Leu Ser His
 130 135 140

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692

SUBSTITUTE SHEET (RULE 26)

577

```

Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn
1      5      10      15
Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr
      20      25      30
Ile Asp Unk Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly
      35      40      45
Val Tyr Gly Val Lys Unk Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser
      50      55      60
Gly Gly Arg Ile Phe Trp Val Trp Unk Unk Unk Phe Leu Ser Cys Ile
65      70      75      80

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

```

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1      5      10      15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
      20      25      30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
      35      40      45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
      50      55      60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65      70      75      80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
      85      90      95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
      100      105      110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
      115      120      125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
      130      135      140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145      150      155      160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
      165      170      175
Leu Val Lys

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

578

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

```

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1      5      10      15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
20     25     30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
35     40     45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
50     55     60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65     70     75     80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
85     90     95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
100    105    110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
115    120    125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
130    135    140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145    150    155    160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
165    170    175
Leu Val Lys

```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694

```

Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile Met Ser
1      5      10      15
Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg Ile Asp
20     25     30
Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu Gly Glu

```

SUBSTITUTE SHEET (RULE 26)

579

```

      35              40              45
Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile Gly Thr
      50              55              60
Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg
      65              70              75

```

(2) INFORMATION FOR SEQ ID NO:695:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695

```

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1              5              10              15
Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
      20              25              30
Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
      35              40              45
Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
      50              55              60
Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
      65              70              75              80
Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
      85              90              95
Gly Asn Asp

```

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696

```

Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr
1              5              10              15

```

SUBSTITUTE SHEET (RULE 26)

580

```

Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg
      20      25      30
Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr
      35      40      45
Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu
      50      55      60
His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu
      65      70      75      80
Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly
      85      90      95
Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp
      100      105      110
Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys
      115      120      125
Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser
      130      135      140
Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser
      145      150      155      160
Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala
      165      170      175
Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro
      180      185      190
Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly
      195      200      205
Asn

```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697

```

Val Gly Ser Leu Lys Phe Leu Asn Ala Met Gly Val Asp Leu Lys Val
1      5      10      15
Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Lys Thr Leu
      20      25      30
Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala Lys Glu
      35      40      45
Val Ile Gln Ala Leu Gln Asn Gln Gly Leu Glu Leu Glu Ile Leu Ser
      50      55      60
Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

581

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698

```

Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu Gln Ile Leu
 1          5          10          15
Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro Met Ile Pro
 20          25          30
His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg Glu Asn Phe
 35          40          45
Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp Phe Met Thr
 50          55          60
Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu Lys Val Asn
 65          70          75          80
Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys Lys Glu Leu
 85          90          95
Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile Tyr Val Pro
100          105          110
Asn Lys Leu Val Asn Phe Val Thr Ala
115          120

```

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699

```

Met Lys Glu Ser Ile Lys Tyr Leu Leu Glu Ser Val Gly Leu Val Leu
 1          5          10          15
Leu Met Ser Val Asn Pro Gly Phe Gly Gly Gln Lys Phe Leu Asp Leu
 20          25          30
Val Leu Glu Lys Cys Leu Lys Val Lys Glu Leu Ile Lys Arg Tyr Asn
 35          40          45
Pro Ser Cys Leu Leu Glu Val Asp Gly Gly Val Asn Asp Lys Asn Ile
 50          55          60
Phe Glu Leu Gln Gln Ala Gly Val Asp Val Val Val Ser Gly Ser Tyr
 65          70          75          80
Ile Phe Glu Ser Lys Asp Unk Lys Leu Ala Ile Glu Gly Leu Gln Asn
 85          90          95

```

SUBSTITUTE SHEET (RULE 26)

582

Val Arg Gln Pro Leu Ala
100

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700

```

Val His Asp Gly Val Leu Gly Trp Val Gly Phe Thr Leu Ile Ala Ser
1          5          10          15
Met Tyr His Met Thr Pro Arg Leu Phe Lys Arg Glu Ile Tyr Ser Gly
          20          25          30
Arg Leu Val Asp Phe Gln Phe Trp Ile Met Thr Leu Gly Ile Val Leu
          35          40          45
Tyr Phe Ser Ser Met Trp Ile Ala Gly Ile Thr Gln Gly Met Met Trp
          50          55          60
Arg Asp Val Asp Gln Tyr Gly Asn Leu Thr Tyr Gln Phe Ile Asp Thr
          65          70          75          80
Val Lys Ala Leu Ile Pro Tyr Tyr Asn Ile Arg Gly Val Gly Gly Leu
          85          90          95
Met Tyr Phe Ile Gly Phe Ile Ile Phe Ala Tyr Asn Ile Phe Met Thr
          100         105         110
Ile Thr Ala Gly Lys Lys Leu Glu Arg Glu Pro Asn Tyr Ala Thr Pro
          115         120         125
Met Ala Lys
          130

```

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701

Met Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser

SUBSTITUTE SHEET (RULE 26)

583

```

1           5           10           15
Ser Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln
20           25           30
Phe Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg
35           40           45
Ala Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile
50           55           60
Glu Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His
65           70           75           80
Arg Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe
85           90           95
Ile Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His
100          105          110
Ser Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu
115          120          125
Leu Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu
130          135          140
Arg Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser
145          150          155          160
Val Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn
165          170          175
Glu Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg
180          185          190
Val Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr
195          200          205
Lys Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys
210          215          220
Arg Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe
225          230          235          240
Ala Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu
245          250          255
Lys Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu
260          265          270
Ile Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Ser Asn Tyr
275          280          285
Ile Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met
290          295          300
Ile Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp
305          310          315          320
Phe Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys
325          330          335
Glu Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro
340          345          350
Ser Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala
355          360          365
Leu Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg
370          375          380
Ile Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu
385          390          395          400
Glu Ala Asp Asn Glu Glu Leu Pro Pro Pro Glu Asn Leu Arg Glu Val
405          410          415
Lys Gly Met Lys Gly Thr Glu Lys Ala Asn Cys Gly Val Lys Glu Lys
420          425          430
Gln Lys Glu Arg Thr Cys Ser Asn Asp
435          440

```

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

584

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702

```

Val Leu Leu Leu Ser Arg Met Gly Ile Ala Phe Ala His Ser Ile Phe
1           5           10           15
Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg Asn Lys
           20           25           30
Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu Ala Met
           35           40           45
Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp
           50           55           60
Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile Met Leu
           65           70           75           80
Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala Gly Thr
           85           90           95
Leu Ala Ser Val Pro Ile Leu Met Lys Arg Pro Leu Leu Val Gly Ile
           100          105          110
Tyr Leu His Val Asn His Gly Tyr Phe Trp Ala Phe His His Leu
           115          120          125

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1           5           10           15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
           20           25           30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
           35           40           45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
           50           55           60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
           65           70           75           80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
           85           90           95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
           100          105          110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp

```

SUBSTITUTE SHEET (RULE 26)

585

```

      115      120      125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
130      135      140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145      150      155      160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
      165      170      175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180      185      190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
195      200      205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
210      215      220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225      230      235      240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
      245      250      255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
      260      265      270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1      5      10      15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
20      25      30
Leu Arg Glu Arg Glu Tyr Leu Ala Glu Thr Ser Glu Leu Lys Asp
35      40      45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
50      55      60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65      70      75      80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
85      90      95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
100      105      110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
115      120      125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
130      135      140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145      150      155      160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

586

```

Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180      185      190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
      195      200      205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
      210      215      220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
      225      230      235      240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu
      245      250      255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
      260      265      270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

```

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1      5      10      15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
      20      25      30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
      35      40      45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
      50      55      60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
      65      70      75      80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
      85      90      95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

```

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1      5      10      15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
20      25      30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
35      40      45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg
50      55      60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
65      70      75      80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
85      90      95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr
100      105      110

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705

```

Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu
1      5      10      15
Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn
20      25      30
Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu
35      40      45
Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg
50      55      60
Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile
65      70      75      80
Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys
85      90      95
Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys
100      105      110
Lys Tyr Ser
115

```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

SUBSTITUTE SHEET (RULE 26)

588

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706

```

Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1          5          10          15
Lys His Ser Val Cys Leu Lys Pro Phe Phe Arg Phe Cys Phe Leu Lys
20          25          30
Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
35          40          45
Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
50          55          60
Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65          70          75          80
Arg Val Ser Asn Ala Tyr
85

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707

```

Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1          5          10          15
Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
20          25          30
Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
35          40

```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

589

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708

```

Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser His
1      5      10      15
Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly Thr Ala Thr Ile Met
20      25      30
Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala Ser Ser Lys Glu Val
35      40      45
Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala Ile Tyr Tyr Gly Tyr
50      55      60
Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp Asn Tyr Leu Lys Leu
65      70      75      80
Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met Val Met Thr Asp Asn
85      90      95
Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val Lys Asp Gly Gly Leu
100     105     110
Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr Ile Tyr Thr Ser Ile
115     120     125
Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn Asp Pro Ile Asn Asn
130     135     140
Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala Gln Ile Gln Gly Val
145     150     155     160
Gln Ser Val Asp Ser Ile Unk Gln Ala Gly Gly Asn Gln Ala Ile Asn
165     170     175
Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser Pro Leu Phe Ala Pro
180     185     190
Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu Thr Thr Ile Ala Gly
195     200     205
Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn Pro Asn Phe Lys Asn
210     215     220
Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr Thr Gln Gln Met Ser
225     230     235     240
Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe Ala Arg Ser Asp Phe
245     250     255
Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg Phe Ala Asp Ala Ile
260     265     270
Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asn Arg Val
275     280     285
Lys Asn Asn Val Trp Ala Thr Gly Val Gly Gly Ala Ser Phe Ile Ser
290     295     300
Gly Gly Thr Unk Thr Leu Tyr Gly Ile Asn Unk Gly Tyr Asp Arg Phe
305     310     315     320
Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr Ser Gly
325     330     335
Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser Asn Val Asn Val Gly
340     345     350
Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu Leu Thr Met Ser Leu
355     360     365
Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile Asn Ser Tyr Asp Pro
370     375     380
Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr Asp Thr Trp Thr Thr
385     390     395     400
Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met Phe Lys Asp Lys Ser
405     410     415

```

SUBSTITUTE SHEET (RULE 26)

590

```

Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr Tyr Tyr Ile Gly Leu
      420      425      430
Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile Tyr Asn Gln Phe Arg
      435      440      445
Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu Thr Ile Asn Phe Ala
      450      455      460
Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser Tyr Tyr Phe Val Ile
      465      470      475      480
Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser Met Gly Asp Lys Met
      485      490      495
Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr Arg Asp Gly Gly Arg
      500      505      510
Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly Glu Ile Arg Leu Phe
      515      520      525
Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala Arg Phe Gly Leu Asp
      530      535      540
Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly Met Unk Unk Unk Phe
      545      550      555      560

```

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

```

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1      5      10      15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
      20      25      30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
      35      40      45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
      50      55      60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
      65      70      75      80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
      85      90      95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
      100      105      110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
      115      120

```

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

591

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

```

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1      5      10      15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
      20      25      30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
      35      40      45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
      50      55      60
Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met
      65      70      75      80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
      85      90      95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
      100      105      110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
      115      120

```

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

```

Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1      5      10      15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
      20      25      30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
      35      40      45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
      50      55      60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
      65      70      75      80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
      85      90      95

```

SUBSTITUTE SHEET (RULE 26)

592

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

```

Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1          5          10          15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
20          25          30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
35          40          45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
50          55          60
Val Asp Ala Ile Gly Leu Pro Ala Pro Unk Lys Arg Glu Arg Lys Arg
65          70          75          80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
85          90          95

```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

```

Leu Pro Ile Ile Leu Unk Val Ile Val Met Met Phe Phe Ser Lys Ile
1          5          10          15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
20          25          30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
35          40          45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
50          55          60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

```

Leu Pro Ile Ile Leu Unk Val Ile Val Met Phe Phe Ser Lys Ile
1          5          10          15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
20          25          30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
35          40          45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
50          55          60
Leu Ile Glu Cys Leu Unk Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65          70          75          80

```

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712

```

Met Glu Ser Asn Gln Ser Leu Pro Met Ala Leu Ile Ser Cys Ser Pro
1          5          10          15
Asn Ala Lys Gly Ala Asp Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu
20          25          30
Leu Ile Glu Arg Asn Phe Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser
35          40          45
Thr Leu Thr Asn Gly Leu Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn
50          55          60
Arg Gly Asn Lys Glu Glu Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu
65          70          75          80
Leu Gln Leu Met Arg Gln Ser Gly Met Gly Ile Asn Gln Val Val Asn
85          90          95

```

SUBSTITUTE SHEET (RULE 26)

594

Gln Ile Leu Arg Asp Lys Ser Lys Ile Ala Pro Ile Val Val Ile Arg
 100 105 110
 Glu Gly Ser Arg Val Phe Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro
 115 120 125
 Ile Pro Arg Glu Asn Glu Val Ile Ala Glu Phe Leu Lys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713

Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro
 1 5 10 15
 Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu
 20 25 30
 Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly
 35 40 45
 Asn Glu Arg
 50

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714

Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
 1 5 10 15
 Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
 20 25 30
 Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
 35 40 45
 Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp

SUBSTITUTE SHEET (RULE 26)

595

```

      50              55              60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65              70              75              80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
      85              90              95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
      100              105              110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala
      115              120              125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg
      130              135              140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu
      145              150              155              160
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln
      165              170              175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr
      180              185              190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
      195              200              205
Ile Lys Ser Gly Thr Leu Leu Ala Ala Gly Thr Leu Met Lys Phe Met
      210              215              220
Lys Thr Leu Trp Cys Val Ser Ile Ile
      225              230

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1              5              10              15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
      20              25              30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
      35              40              45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
      50              55              60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
      65              70              75              80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
      85              90              95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
      100              105              110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
      115              120              125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
      130              135              140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
      145              150              155              160

```

SUBSTITUTE SHEET (RULE 26)

596

```

Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
      165      170      175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
      180      185      190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
      195      200      205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
      210      215      220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
      225      230      235      240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
      245      250      255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
      260      265

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

```

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1      5      10      15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
      20      25      30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
      35      40      45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
      50      55      60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
      65      70      75      80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
      85      90      95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
      100      105      110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
      115      120      125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
      130      135      140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Asp Glu Pro Leu Asn
      145      150      155      160
Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
      165      170      175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
      180      185      190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
      195      200      205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
      210      215      220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile

```

SUBSTITUTE SHEET (RULE 26)

597

```

225          230          235          240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
          245          250          255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
          260          265

```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716

```

Met Lys Glu Ile Val Thr Ile Glu Asn Val Ser Phe Asn Tyr His Asn
1          5          10          15
Arg Ala Ile Phe Lys Asp Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe
          20          25          30
Leu Cys Val Leu Gly Glu Ser Gly Lys Ser Thr Leu Leu Gly
          35          40          45
Leu Ile Leu Gly Leu Leu Lys Pro Ser Leu Gly Ser Val Lys Ile Phe
          50          55          60
Asn Glu Thr Leu Ser Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr
          65          70          75          80
Ile Ala Gln Gly Asn Ser Leu Phe Pro His Leu Asn Ala Leu Gln Asn
          85          90          95
Met Thr Phe Cys Leu Asn Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln
          100          105          110
Lys Glu Ala Lys Ala Leu Ala Leu Lys Met Gly Leu Asp Glu Ser Leu
          115          120          125
Met Asp Lys Phe Pro Asn Glu Leu Ser Gly Gly Gln Ala Lys Glu Trp
          130          135          140
Ala Leu Leu Gly Gly Leu Ser Thr Gly Gln Asn Ser Phe Tyr
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

598

(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717

```

Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly Leu Ser Glu
1      5      10      15
Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile Leu Ser Leu
20     25     30
Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser His Tyr Leu
35     40     45
Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro Asn Ala Pro
50     55     60
Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe Lys Lys Thr
65     70     75     80
Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val Val Ala Leu
85     90     95
Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys Ile Phe Asp
100    105    110
Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu Ile Phe Leu
115    120    125
Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala Leu Pro Leu
130    135    140
Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu Asp Lys Asp
145    150    155    160
Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr Ala Phe Phe
165    170    175
Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys Leu Lys
180    185    190

```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718

```

Met Val Leu Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val
1      5      10      15
Leu Ser Glu Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp
20     25     30
Val Ala Asp Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu
35     40     45
Lys Lys Lys Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn
50     55     60
Lys Ile Ala Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr
65     70     75     80
Ile Leu Ser Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro
85     90     95
Lys Asp Leu Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys
100    105    110
Asp Ile Val Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr

```

SUBSTITUTE SHEET (RULE 26)

599

```

      115      120      125
Ala Leu Ile Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp
 130      135      140
Phe Thr Phe Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val
145      150      155      160
Thr Phe Asn Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe
      165      170      175
Leu Asn Unk Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala
      180      185      190
Leu Glu Trp Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro
      195      200      205
Lys Glu Ala Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu
      210      215      220
Thr Gly Cys Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys
225      230      235      240
Lys Gly Arg

```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719

```

Val Ser Glu Val Ala Ser Val Gly Gly Phe Val Lys Asp Tyr Glu Val
1      5      10      15
Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr Asn Leu Ser Leu Glu Gln
      20      25      30
Val Ala Asn Ala Ile Lys Asn Ser Asn Asn Asp Thr Gly Gly Gly Val
      35      40      45
Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile Arg Ser His Gly Tyr Ile
      50      55      60
Gln Ser Leu Asn Asp Leu Glu Glu Ile Val Val Lys Lys Glu Gly Ala
      65      70      75      80
Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser Val Arg Leu Ala Pro Lys
      85      90      95
Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly Asp Lys Glu Val Val Gly
      100      105      110
Gly Ile Val Met Val Arg Tyr His Ala Asp Thr Tyr Lys Val Leu Lys
      115      120      125
Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln Ala Ser Asn Pro Asp Val
      130      135      140
Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu Leu Ile Glu Lys Gly Ile
      145      150      155      160
Asp Asn Leu Ile His Thr Leu Ile Glu Glu Ser Val Ile Val Leu Val
      165      170      175
Ile Ile Ala Ile Phe Leu Leu His Phe Arg Ser Ala Leu Val Val Ile
      180      185      190
Ile Thr Leu Pro Leu Arg Val Cys Ile Ser Phe Leu Leu Met Ser Tyr
      195      200      205

```

SUBSTITUTE SHEET (RULE 26)

600

Phe Asn Ile Glu Ala Ser Ile Met Ser Leu Gly Gly Ile Ala Ile Ala
 210 215 220
 Ile Gly Ala Met Val Asn Ala Ala Ile Val Met Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720

Val Glu Thr Phe Leu Arg Ile Phe Glu Lys Asp Ile Phe Asn Thr Pro
 1 5 10 15
 Tyr Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys
 20 25 30
 Gly Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys
 35 40 45
 Ser Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Gln Ser Glu
 50 55 60
 Gln Ala Lys Asn Leu Lys Ile Ala Lys Lys Lys Cys Glu Glu Ile Ile
 65 70 75 80
 Lys Tyr Ala Asn Glu Lys Lys Thr Gln Val Glu Glu Ala Phe Leu Lys
 85 90 95
 Val Ala Glu Phe Leu Glu Lys Val Glu Lys Leu His Glu Lys Asn Lys
 100 105 110
 Leu Glu Glu Leu Asp Phe Glu Glu Leu Glu Asn Leu Ser Ala Glu Ile
 115 120 125
 Asp Asn Val Lys Glu Leu Phe Asp Asp Lys Arg Phe Asn Ser Tyr Phe
 130 135 140
 Met Asp Ala Ile Gln Ser Tyr Ile Phe His Gln Glu Leu His Ile Ala
 145 150 155 160
 Glu Ile Val Cys Lys Lys Thr Ser Asn Glu Asp Gly Ile Lys Gly
 165 170 175

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

601

(A) NAME/KEY: misc_feature
(B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721

```

Met Lys Thr Pro Cys Asn Ala Tyr Phe Leu Lys Thr Pro Pro Lys Asn
1      5      10      15
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu Leu
20      25      30
Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Unk Lys
35      40      45
Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu Gly
50      55      60
Glu Ile Leu Ser Leu Leu Glu Lys His His Ile Pro Ile Lys Arg
65      70      75      80
Ala Phe Gly Ile Gly Gly Gly Thr Met Asn Ile His Pro Ala Leu Ile
85      90      95
Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp Val
100      105      110
Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr Ile
115      120      125
Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu Leu
130      135      140
Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala Gln
145      150      155      160
Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro Asn
165      170      175
Phe Asp Phe Gly Ala Glu Unk Asp Phe Phe Glu Arg Glu Asp Ala Phe
180      185      190
Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His Glu
195      200      205
Met Unk Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser Leu Ile Arg Unk
210      215      220
Thr Leu
225

```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722

```

Val Met Val Tyr Lys Leu Pro Lys His Gln Gln Asn Lys Val Met Ile
1      5      10      15
Leu Gly Leu Gly Leu Ala Met Ile Thr Arg Ile Gly Leu Leu Gly Ser
20      25      30
Leu Phe Phe Ile Ser His Leu Gln Lys Pro Leu Phe Ala Ile Ala Gly
35      40      45
Met Ser Phe Ser Trp Arg Asp Val Val Leu Leu Leu Gly Gly Ala Phe
50      55      60

```

SUBSTITUTE SHEET (RULE 26)

602

Leu Ala Phe Lys Ala Leu Val Glu Leu Lys Arg Ala Asp Leu Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
 1 5 10 15
 Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
 20 25 30
 Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
 35 40 45
 Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
 1 5 10 15
 Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
 20 25 30
 Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
 35 40 45
 Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:724:

SUBSTITUTE SHEET (RULE 26)

603

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724

```

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
1          5          10          15
Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
          20          25          30
Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
          35          40          45
Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
50          55          60
Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
65          70          75          80
Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala
          85          90          95
Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
          100          105          110
Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
          115          120          125
Val Val Gly Gly Phe Leu Gly Met Glu His
130          135

```

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724

```

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
1          5          10          15
Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala
          20          25          30
Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
          35          40          45

```

SUBSTITUTE SHEET (RULE 26)

604

```

Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
 50          55          60
Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
 65          70          75          80
Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala
      85          90          95
Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met
      100          105          110
Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
      115          120          125
Val Val Gly Gly Phe Leu Gly Met Glu His
      130          135

```

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725

```

Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu Ala Ile Ser Leu Cys
 1          5          10          15
Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val Glu Arg Gly Met Ala
      20          25          30
Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys Phe Met Cys Asp Ile
      35          40          45
Val Leu Met Ser Met Gly Val Phe Gly Val Gly Ala Tyr Phe Ala Lys
      50          55          60
Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe Gly Ala Val Phe Thr
      65          70          75          80
Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu Phe Gln Thr Phe Lys
      85          90          95
Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser Leu Lys Lys Thr Leu
      100          105          110
Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro Gln Val Tyr Leu Glu
      115          120          125
Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser Phe Asn Leu Val Gln
      130          135          140
Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala Ala Phe Ser Trp Leu
      145          150          155          160
Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly Ser Lys Leu Leu Asn
      165          170          175
Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe Val Thr Ala Ile Met
      180          185          190
Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe Leu Ala Leu Leu Ser
      195          200          205
Lys Thr
      210

```

(2) INFORMATION FOR SEQ ID NO:726:

SUBSTITUTE SHEET (RULE 26)

605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726

Val	Lys	Pro	Lys	Ser	Met	Lys	Glu	Lys	Leu	Arg	Gly	Ala	Met	Val	Asn
1				5					10					15	
Ile	Leu	Arg	Ile	Lys	Met	Ile	Glu	Ile	Ser	Glu	Trp	Leu	Gln	Lys	Leu
		20					25						30		
Asp	Asp	Ala	Leu	Asp	Lys	Val	Val	Ala	Lys	Lys	Glu	Pro	Glu	Ser	Phe
		35					40					45			
Leu	Lys	Pro	Ile	Ile	Ser	Pro	Ile	Glu	Asp	Tyr	Gln	Lys	Ser	Val	Arg
	50				55					60					
Gln	Ile	Gln	Ala	Gln	Phe	Thr	Asp	Ala	Pro	Lys	Phe	Asn	Glu	Glu	Gly
65					70				75						80
Ala	Tyr	Pro	Gln	Phe	Leu	Ser	Cys	Gly	Leu	Leu	Gln	Val	Arg	Gly	Lys
				85				90					95		
Asn	Gly	Ala	Asn	Met	Glu	Phe	Leu	Leu	Pro	Lys	Val	Tyr	Pro	Phe	Pro
		100						105					110		
Pro	Lys	Ser	Leu	Tyr	Ile	Glu	His	Glu	Lys	Asp	Gly	Gln	Phe	Leu	Arg
		115					120					125			
Glu	Met	Leu	Met	Arg	Leu	Leu	Ser	Ser	Ala	Pro	Leu	Val	Gln	Leu	Glu
	130				135					140					
Val	Ile	Leu	Ile	Asp	Ala	Leu	Ser	Leu	Gly	Gly	Ile	Phe	Asn	Leu	Ala
145					150					155					160
Arg	Arg	Leu	Leu	Asp	Lys	Asn	Asn	Asp	Phe	Ile	Tyr	Gln	Gln	Arg	Ile
			165						170				175		
Leu	Thr	Glu	Ser	Lys	Glu	Ile	Glu	Glu	Ala	Leu	Lys	His	Leu	His	Glu
		180						185					190		
Tyr	Leu	Lys	Val	Asn	Leu	Gln	Glu	Lys	Leu	Ala	Gly	Phe	Arg	Asp	Phe
	195					200						205			
Val	His	Tyr	Asn	Glu	Asn	Ala	Lys	Asp	Ser	Leu	Pro	Leu	Lys	Ala	Leu
	210					215					220				
Phe	Leu	Ser	Gly	Val	Asp	Ala	Leu	Ser	Lys	Asp	Ala	Leu	Tyr	Tyr	Leu
225				230						235					240
Glu	Lys	Ile	Met	Arg	Phe	Gly	Ser	Lys	Asn	Gly	Val	Leu	Ser	Phe	Val
			245						250				255		
Asn	Leu	Glu	Ser	Glu	Lys	Asn	Asn	Gln	Ser	Ala	Glu	Asp	Leu	Lys	Arg
		260					265						270		
Tyr	Ala	Glu	Phe	Phe	Lys	Asp	Arg	Thr	Ser	Phe	Glu	Unk	Leu	Lys	Tyr
	275					280						285			
Leu	Asn	Val	Glu	Ile	Ile	Ser	Asp								
	290					295									

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

606

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727

```

Val Leu Ile Ser Val Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile
1          5          10          15
Gly Thr Asn Phe Lys Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser
          20          25          30
Ala Glu Ile Asn Ile Gly Asn Gln Val Ile Thr Ser Gly Leu Asp Gly
          35          40          45
Ile Phe Gly Ala Gly Val Phe Val Gly Glu Val Ser Ser Val Glu Asp
          50          55          60
His Tyr Thr Tyr Lys Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu
65          70          75          80
Ala Lys Leu Leu Arg His Val Phe Leu Ser Gly Val Lys Asn
          85          90

```

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728

```

Met Glu Ala Gln Leu Arg Phe Thr Gly Val Gly Gly Gln Gly Val Leu
1          5          10          15
Leu Ala Gly Glu Ile Leu Ala Glu Ala Lys Ile Val Ser Gly Gly Tyr
          20          25          30
Gly Thr Lys Thr Ser Thr Tyr Thr Ser Gln Val Arg Gly Gly Pro Thr
          35          40          45
Lys Val Asp Ile Leu Leu Asp Lys Asp Glu Ile Ile Phe Pro Tyr Ala
          50          55          60
Lys Glu Gly Glu Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr
65          70          75          80
Asn Gln Phe

```

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

607

(A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729

```

Met Gln Ala Trp Val Asp Lys Pro Val Leu Leu Glu Pro Asp Ser Asn
1      5      10      15
Ala Gln Tyr Ala Val Ile Glu Ile Asp Val Ala Glu Ile Thr Glu
20      25      30
Pro Ile Leu Ala Cys Pro Asn Asp Pro Asp Asp Val Ala Thr Leu Ser
35      40      45
Glu Val Leu Ala Asp Thr Thr Gly Lys Arg Pro His Ala Ile Asp Glu
50      55      60
Val Phe Ile Gly Ser Cys Met Thr Asn Ile Gly His Phe Arg Ala Phe
65      70      75      80
Gly Glu Ile Val Lys Asn Ala Pro Pro Ser Gln Ala Arg Leu Trp Val
85      90      95
Val Pro Pro Ser Lys Met Asp Glu Gln Glu Leu Ile Asn Glu Gly Tyr
100     105     110
Tyr Ala Ile Phe Gly Ala Ala Gly Ala Arg Thr Glu Val Pro Gly Cys
115     120     125
Ser Leu Cys Met Gly Asn Gln Ala Arg Val Arg Asp Asn Ala Val Val
130     135     140
Phe Ser Thr Ser Thr Arg Asn Phe Asp Asn Arg Met Gly Arg Gly Ala
145     150     155     160
Lys Val Tyr Leu Gly Ser Ala Glu Leu Gly Ala Ala Cys Ala Leu Leu
165     170     175
Gly Arg Ile Pro Thr Lys Glu Glu Tyr Met Asn Leu Val Ser Glu Lys
180     185     190
Leu Glu Ser Gln Lys Asp Lys Ile Tyr Arg Ser
195     200

```

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730

SUBSTITUTE SHEET (RULE 26)

608

```

Val Gly Asn Ala Gly Val Ala Leu Ala Gly Leu Met Ser Asp Glu Ile
1      5      10      15
Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile Lys Gly Phe Lys Lys His
20     25     30
Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys Glu Ile Asp Thr Ser Ser
35     40     45
Leu Ile Ser Val Glu Gly Asn Val Glu Gly Tyr Glu Thr Phe Ser Asp
50     55     60
Ser Leu Phe Leu Leu Ser Lys Glu Arg Ile Glu Glu Ala Leu His Tyr
65     70     75     80
Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser Tyr Gly Ala Lys Ile Lys
85     90     95
His Ala Val Ser Leu Asn His Ser Gln Val Lys Leu Lys Gln Ile Asn
100    105    110
Lys Gln Asp Ala Ile Val Arg Ile Lys Ser Met Phe Ser Pro Arg Ser
115    120    125
Asn His Ala Lys Asp Leu Lys Asn Leu Gln Lys Asn Leu Ile Arg Phe
130    135    140
Lys Glu Asp Phe Phe Thr His Leu Asn Thr Pro Cys Lys Thr Lys Gln
145    150    155    160
Glu Ala Phe Glu Trp Val Asp Ser Leu Ser Gly Phe Cys Gln Thr Ala
165    170    175
Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu Phe Glu Gly Ser Val Ala
180    185    190
His Ile Leu Gln Ser Val Leu Ile Val Ser Leu His Leu Lys Glu Asn
195    200    205
Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys Thr Pro
210    215    220

```

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731

```

Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1      5      10      15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
20     25     30
Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
35     40     45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
50     55     60
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65     70     75     80
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
85     90     95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
100    105    110
Ala Ile Ile Unk

```

SUBSTITUTE SHEET (RULE 26)

609

115

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731

```

Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1           5           10           15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
20           25           30
Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
35           40           45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
50           55           60
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65           70           75           80
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
85           90           95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
100          105          110
Ala Ile Ile Unk
115

```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732

```

Met Gln Lys Ser Ile Phe Lys Ile Thr Leu Leu Leu Val Phe Leu Phe
1           5           10           15
Leu Arg Asn Ala Val Gly Leu Asp Asp Lys Lys Ala Ala Pro Lys Ser
20           25           30

```

SUBSTITUTE SHEET (RULE 26)

610

```

Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
   35           40           45
Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
   50           55           60
Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu
   65           70           75           80
Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met
   85           90           95
Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn
  100           105           110
Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe
  115           120           125
Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu
  130           135           140
His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro
  145           150           155           160
Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala
  165           170           175
Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser
  180           185           190
Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met
  195           200           205
Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr
  210           215           220
Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys
  225           230           235           240
Asn Lys Pro Ala Leu Val Glu Lys
                245

```

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid.
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733

```

Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser Tyr Lys Val Phe
  1           5           10           15
Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys Ala Leu Ile Ile
  20           25           30
Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr Leu Leu Glu Arg
  35           40           45
Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu Ser Gly Glu Lys
  50           55           60
Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn Asn Ala Phe Glu
  65           70           75           80
Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu Gly Gly Gly Val
  85           90           95
Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr Phe Arg Gly Ile
  100           105           110
Asp Phe Ile Asn Ile Pro Tyr Asp Phe Thr Arg Ser Ser Gly Cys Glu

```

SUBSTITUTE SHEET (RULE 26)

611

```

      115              120              125
Arg Gly Gly Glu Asn Arg Asp Gln His Ala Leu Trp Gln Glu Pro Asn
  130              135              140
Arg Ile Val Pro Pro Ala
  145              150

```

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

```

Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
 1              5              10              15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
 20              25              30
Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
 35              40              45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
 50              55              60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
 65              70              75              80
Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
 85              90              95
Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
 100             105             110
Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
 115             120             125
Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
 130             135             140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
 145             150             155             160
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
 165             170             175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
 180             185             190
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
 195             200             205
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Glu Lys Unk
 210             215             220
Lys Arg Leu
 225

```

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

612

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

```

Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Unk
1      5      10      15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
20     25     30
Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
35     40     45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
50     55     60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
65     70     75     80
Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
85     90     95
Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
100    105    110
Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
115    120    125
Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
130    135    140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
145    150    155    160
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
165    170    175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
180    185    190
Unk Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Unk
195    200    205
Phe Lys Asn Unk Unk Ala Leu Thr Pro Unk Asp Leu Ile Glu Lys Unk
210    215    220
Lys Arg Leu
225

```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735

SUBSTITUTE SHEET (RULE 26)

613

```

Met Arg Ile Leu His Tyr Gly Gly Glu Leu Pro Cys Asp Cys Pro Lys
1      5      10      15
Arg Ile Ala Gly Leu Asp Phe Ala Leu Lys Ile Leu Thr Asn Ile Thr
20      25      30
Ser Asp His Leu Asp Phe His Gln Asn Ile Glu Asn Tyr Arg Asp Ala
35      40      45
Lys Asn Ser Phe Phe Lys Asp Glu Gly Leu Lys Val Ile Asn Arg Asp
50      55      60
Glu Thr Asn Ala Leu Phe Asn Pro Ile Asn Ala Arg Thr Tyr Ala Leu
65      70      75      80
Asp Lys Lys Ala His Leu Asn Val Gln Ala Phe Ser Leu Asn Pro Ser
85      90      95
Ile Ser Ala Ser Leu Cys Tyr Gln His Asp Leu Arg Asp Pro Asn Leu
100     105     110
Lys Glu Thr Ala Leu Ile His Ser Pro Leu Leu Gly Arg Tyr Asn Leu
115     120     125
Tyr Asn Ile Leu Ala Gly Val Leu Gly Val Lys Leu Leu Thr Gln Leu
130     135     140
Pro Leu Glu Thr Ile Ala Pro Leu Leu Glu Asn Phe Tyr Gly Val Lys
145     150     155     160
Gly Arg Leu Glu Ile Val His Ser Lys Pro Leu Val Val Val Asp Phe
165     170     175
Ala His Thr Thr Asp Gly Met Gln Gln Val Phe
180     185

```

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736

```

Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr Phe Gln
1      5      10      15
Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly Thr Ala
20      25      30
Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu Val Val
35      40      45
Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn Asp Leu
50      55      60
Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu Lys Ile
65      70      75      80
Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr Ala Ser
85      90      95
Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu Arg Ile
100     105     110
Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala Glu Ile
115     120     125
Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr Asn Met
130     135     140

```

SUBSTITUTE SHEET (RULE 26)

614

Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys Glu Leu
 145 150 155 160
 Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Ile
 165 170 175
 Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Val
 180 185 190
 Ser Gln Phe Tyr Leu Ser
 195

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737

Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys Ala
 1 5 10 15
 Thr Lys Glu Ile Ala Val Val Val Lys Ser Met Gln Gln Glu Ala Asn
 20 25 30
 Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Gly Ser Ile
 35 40 45
 Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met Ile
 50 55 60
 Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg Val
 65 70 75 80
 Phe Cys Gly Unk Ala Lys Leu Asp His Val Val Phe Lys Asn Asn Leu
 85 90 95
 Tyr Gly Met Val Unk Leu Val Ser Ile Pro Leu Thr Leu Pro Ala His
 100 105 110
 Lys Ser Unk Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu
 115 120 125
 Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala
 130 135 140
 Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp
 145 150 155 160
 His Val Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu
 165 170 175
 Asp Ser Ala Lys His Val Lys Glu Asn Ile Asp Lys Met Phe Tyr Glu
 180 185 190
 Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly Glu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

615

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738

```

Met Asn Thr Ser Lys Lys Leu Gly Asn Pro Leu Leu Phe Leu His Asp
1      5      10      15
Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser Met Gly Gly Trp Ala
20      25      30
Thr Ser Lys Ile Tyr Gln Phe Glu Ser Ala Leu Glu Pro Ile His Phe
35      40      45
Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe Leu Asn Leu Ser His
50      55      60
Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp Gly Gly Phe Met Leu
65      70      75      80
Pro Leu Tyr His Glu Leu Ala Thr Gln Tyr Pro Leu Leu Leu Lys Phe
85      90      95
Asp Gln Gln Asn Asn Pro Arg Glu Leu Leu Arg Pro Asn Thr Leu Asn
100     105     110
His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys Asp Cys Ala Val Met
115     120     125
Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu Met Leu Glu Thr Cys
130     135     140
Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser Thr Asn Leu Lys Asn
145     150     155     160
Leu Asp Asp Ser Leu Asn Leu Leu Asn Leu Asn Gly Ile Leu Tyr Leu
165     170     175
Ile His Asn Pro Ser Asp Leu Ser Leu Arg Arg Lys Glu Leu Trp Leu
180     185     190
Ser Lys Leu Glu Asn Gln Gln Leu Ile
195     200

```

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739

```

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1      5      10      15
Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
20      25      30

```

SUBSTITUTE SHEET (RULE 26)

616

```

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
   35                               40                               45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
   50                               55                               60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
   65                               70                               75                               80
Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
   85                               90                               95
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
  100                               105                               110
Asp Gly Met Thr Val Arg Glu Leu Ser Arg Trp Cys His Asn His
  115                               120                               125

```

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740

```

Val Asn Val Gly Val Pro Phe Ser Tyr Gln Val Ser Ala Thr Phe Gln
  1                               5                               10                               15
Asn Ser Arg Leu Ser Ser Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu
   20                               25                               30
Glu Lys Pro Leu Ile Glu Ser Ser Ala Asn Lys Ile Ala Asp Ile Phe
   35                               40                               45
Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser Phe Leu Leu Trp Gln
   50                               55                               60
Phe Gly Leu Gly Gly Asn Phe Glu Lys Ser Phe Asn Gly Val Tyr
   65                               70                               75

```

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741

SUBSTITUTE SHEET (RULE 26)

617

```

Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys
1           5           10           15
Val Gly Phe Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile
          20           25           30
Gln Asn Arg Ser Tyr Leu Met Ser Tyr Glu Leu Ser Phe Leu Arg
          35           40           45
Asn

```

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742

```

Met Val Gln Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe
1           5           10           15
Lys Asn Ala Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr
          20           25           30
Lys Glu Asn Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln
          35           40           45
Glu Asp Val Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu
          50           55           60
Lys Asp Ile Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp
          65           70           75           80
Asn Gln Leu Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr
          85           90           95
Ser Ala Ile Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly
          100          105          110
Val Lys Ala Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala
          115          120          125
Pro Lys Pro Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val
          130          135          140
Met Ile Ser Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val
          145          150          155          160
Asn Leu Ser Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu
          165          170          175
Asp Ala Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln
          180          185          190
Asn Ala Asp Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu
          195          200          205
Lys Ala Phe Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu
          210          215          220
Gly Gln Ser Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu
          225          230          235          240
Gln Met Leu Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val
          245          250          255
Asp Met Pro Pro Arg Asn Arg Arg Cys Ala Ala His Ala Ala Gln Ala
          260          265          270

```

SUBSTITUTE SHEET (RULE 26)

618

```

Val Pro Leu Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser
275      280      285
Leu Asp Asp Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile
290      295      300
Pro Ile Ala Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His
305      310      315      320
Cys Lys Lys Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu
325      330      335
Leu Glu Ala Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro
340      345      350
Lys Val Arg Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His
355      360      365
Pro Thr Ser Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu
370      375      380
Ser Ala Phe Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys
385      390      395      400
Asp Ile Gln Pro Thr Gln Thr His Ala Tyr Ser His
405      410

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743

```

Met Gly Val Val Ile Gly Glu Thr Thr Glu Ile Gly Asp Asp Val Thr
1      5      10      15
Ile Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Phe Lys Gly Lys
20      25      30
Arg His Pro Thr Leu Gly Asn Arg Val Val Val Gly Ala Gly Ala Lys
35      40      45
Val Leu Gly Ala Ile Cys Val Gly Asp Asp Val Arg Ile Gly Ala Asn
50      55      60
Ala Val Val Leu Ser Asp Leu Pro Thr Gly Ser Thr Ala Val Gly Ala
65      70      75      80
Lys Ala Lys Thr Ile Thr Lys Asp Arg
85

```

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

619

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744

```

Met Leu Ser Phe Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg
1          5          10          15
Leu Leu Thr Ala Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp
20          25          30
Leu Glu Ile Gln Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys
35          40          45
Ile Gln Ala Leu Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys
50          55          60
Val Val Ser Lys Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn
65          70          75          80
Ala Asn Val Ser Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn
85          90          95
Met Ser Leu Gly Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu
100         105         110
Thr Gln Ser Lys Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu
115         120         125
Leu Lys Lys Thr Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly
130         135         140
Ile Glu Asn Tyr Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala
145         150         155         160
Ile Lys Asn Leu Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser
165         170         175
Pro Asp Leu Ile Glu Ile Asp Lys Leu Glu Asn Leu Lys Ile Ala Asn
180         185         190

```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

```

Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1          5          10          15
Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
20          25          30
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
35          40          45
Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
50          55          60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

620

Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
 85 90 95
 Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
 1 5 10 15
 Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
 20 25 30
 Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
 35 40 45
 Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
 50 55 60
 Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
 65 70 75 80
 Pro Lys Asp Leu Unk Gln Ala Lys Met Gln Phe Unk Met Leu Gln Asn
 85 90 95
 Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746

Val Pro Ala Val Gly Gly Ala Leu Ile Trp Unk Unk Ile Unk Ile Tyr
 1 5 10 15
 Glu Leu Tyr His Gly Unk Val Asn Glu Unk Ile Phe Unk Val Leu Tyr

SUBSTITUTE SHEET (RULE 26)

621

```

      20      25      30
Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile Lys Pro Ile
      35      40      45
Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr Leu Lys Ile
      50      55      60
Asn Glu Ile Leu Ile Phe Ser Met Ile Ala Gly Ile Ser Gln Phe
      65      70      75      80
Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala Phe Phe Ile
      85      90      95
Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys Glu Gln Lys
      100      105      110
Thr Cys Glu Cys
      115

```

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747

```

Val Val Val Ile Ile Leu Val Val Val Ile Ile Gln Asn Ser Ser Ser
1      5      10      15
Leu Lys Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys
      20      25      30
Asn Asn Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu
      35      40      45
Pro Thr Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly
      50      55      60
Lys Glu Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys
      65      70      75      80
Arg Asp Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser
      85      90      95
Phe Gln Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His
      100      105      110
Arg Leu Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn
      115      120      125
His Gln Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr
      130      135      140
Glu Pro Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala
      145      150      155      160
Leu Gln Gln

```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

622

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748

```

Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile
1           5           10           15
Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp Met
          20           25           30
Ser Gln His Lys Asp Asn Leu Gly
          35           40

```

(2) INFORMATION FOR SEQ ID NO:749:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749

```

Val Ala Gly Ser Phe Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln
1           5           10           15
Phe Val Ser Val Phe Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser
          20           25           30
Gln Asn Ala Thr Gln Lys Gln Lys Lys Lys Ser Leu Cys
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:750:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

623

(A) NAME/KEY: misc_feature
(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750

```

Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala
1      5      10      15
Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr
      20      25      30
Val Lys Ile Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn
      35      40      45
Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg
      50      55      60
Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu
65      70      75      80
Ile Thr Glu Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys
      85      90      95
Gly Met Pro Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu
      100      105      110
Ser Pro Leu Phe Ser Met
      115

```

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751

```

Met Ala Val Leu Lys Lys Met Ile Gly Leu Val Ala Val Leu Ser Val
1      5      10      15
Leu Leu Ala Arg Asp Asn Pro Phe Glu Pro Glu Ile Asn Ser Lys Asn
      20      25      30
Leu Gln Gly Gly Phe Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile
      35      40      45
His Val Asp Leu Pro Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu
      50      55      60
Thr Tyr Gln Asp Ile Asp Gly Ser Ile His Ser Lys Val Val Gly Ile
65      70      75      80
Asp Lys Ser Ile Asp Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr
      85      90      95
Leu Asn Gln Asp Ala Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp
      100      105      110
Phe Leu Met Ala Asn Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile
      115      120      125
Leu Arg Ser Phe Val Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr
      130      135      140
Gln Lys Gly Pro Leu Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys
145      150      155      160
Phe Phe Ser His Ile Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

624

Thr Leu Ile Leu Asp Gly Lys Tyr Arg Tyr Leu Leu Glu Glu Lys Asn
 180 185 190
 Gly Ala Tyr Glu Leu Lys Leu Lys
 195 200

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val
 1 5 10 15
 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly
 20 25 30
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu
 35 40 45
 Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr Gln
 50 55 60
 Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
 1 5 10 15
 Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
 20 25 30
 Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
 35 40 45
 Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala

SUBSTITUTE SHEET (RULE 26)

625

```

      50              55              60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp
65              70              75              80
Glu Lys Ile Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
      85              90              95
Cys

```

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

```

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1              5              10              15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
      20              25              30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
      35              40              45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala
      50              55              60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp
65              70              75              80
Glu Lys Ile Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile
      85              90              95
Cys

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

SUBSTITUTE SHEET (RULE 26)

626

```

Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
1      5      10      15
Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
20      25      30
Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
35      40      45
Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
50      55      60
Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
65      70      75      80
Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln
85      90      95
Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Glu Phe Leu
100     105     110
Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
115     120     125
Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
130     135     140
Ser
145

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

```

Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
1      5      10      15
Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
20      25      30
Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
35      40      45
Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
50      55      60
Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
65      70      75      80
Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln
85      90      95
Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Glu Phe Leu
100     105     110
Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
115     120     125
Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
130     135     140
Ser
145

```

(2) INFORMATION FOR SEQ ID NO:755:

SUBSTITUTE SHEET (RULE 26)

627

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755

```

Val Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr Lys Ile Ala
1          5          10          15
Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu Ser Asp Glu
20          25          30
Unk Unk Lys Lys Ile Asn Unk Leu Val Lys Gln Ala Ile Gly Asp Asn
35          40          45
Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu Phe Asn Pro
50          55          60
Met Val Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys Ile Ile Tyr
65          70          75          80
Lys Thr Gln Lys Ile Leu Gly Leu Phe Met Phe Leu Ile Lys Val Tyr
85          90          95
Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val Ile Val Pro
100         105         110
Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp Lys Glu Val
115         120         125
Lys Ser Met Phe Glu Glu Met Asn Glu Glu Glu Asp Glu Leu Asn Lys
130         135         140
Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly Leu Asn Ala
145         150         155         160
Ser Phe Ser Glu Glu Glu Val Arg Tyr Glu Ile Ile Leu Glu Lys Ile
165         170         175
Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr Leu Phe Lys
180         185         190
Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys Gly
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:756:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...98

SUBSTITUTE SHEET (RULE 26)

628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756

```

Val Cys Phe Ile Leu Pro Phe Cys Leu Gly Val Leu Gly Thr Gln Ile
1           5           10           15
Phe Lys Gln Glu Thr Pro Arg Gln Leu Pro Ile Val Val Val Asp Leu
20           25           30
Asp Lys Thr Thr Thr Ser His Gln Val Ala Phe Glu Leu Gly Ala Thr
35           40           45
Ser Ala Val Glu Ile Lys Tyr Gln Val Thr Ser Leu Ser Glu Ala Lys
50           55           60
Arg Phe Leu Asn Ser Ala Glu Val Tyr Gly Ala Leu Ile Leu Pro Lys
65           70           75           80
Asp Leu Glu Arg Lys Ile Lys Met Gly Arg Lys Val Unk Phe Ala Leu
85           90           95
Leu Leu

```

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757

```

Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe Leu
1           5           10           15
Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu Thr
20           25           30
Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr Leu
35           40           45
Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys Asn
50           55           60
Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu Gly
65           70           75           80
Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr His
85           90           95
Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu Asp
100          105          110
Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr Asn
115          120          125
Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn Gly
130          135          140
Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn Ile
145          150          155          160
Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val Val
165          170          175
Ile Tyr Ile Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu Tyr
180          185          190
Phe Phe Lys Lys Ser
195

```

SUBSTITUTE SHEET (RULE 26)

629

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758

```

Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1           5           10           15
Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
20           25           30
Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
35           40           45
Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
50           55           60
Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
65           70           75           80
Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
85           90           95
Ser Val Val Thr Ile Ala Glu Unk Phe Arg Ile Ala Gln Gln Lys Unk
100          105          110
Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Glu Unk Ala Leu Ile
115          120          125
Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
130          135          140
Lys Ile Leu Asn
145

```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758

```

Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1           5           10           15

```

SUBSTITUTE SHEET (RULE 26)

630

```

Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
      20      25      30
Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
      35      40      45
Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
      50      55      60
Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
      65      70      75      80
Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
      85      90      95
Ser Val Val Thr Ile Ala Glu Unk Phe Arg Ile Ala Gln Gln Lys Unk
      100      105      110
Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Glu Unk Ala Leu Ile
      115      120      125
Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
      130      135      140
Lys Ile Leu Asn
145

```

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759

```

Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys Phe Gly Phe Ile
1      5      10      15
Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr Lys Glu Asn Met Thr Glu
      20      25      30
Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu
      35      40      45
Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu Lys Glu Glu Asn Glu Val
      50      55      60
Ala Lys Lys Ile
65

```

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

```

Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1      5      10      15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
      20      25      30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
      35      40      45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
      50      55      60
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
      65      70      75      80
Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu
      85      90      95
Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
      100      105      110
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
      115      120      125
Val Asn Leu Phe Lys Thr
130

```

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

```

Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1      5      10      15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
      20      25      30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
      35      40      45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
      50      55      60
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
      65      70      75      80
Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu
      85      90      95
Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
      100      105      110
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln
      115      120      125
Val Asn Leu Phe Lys Thr
130

```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761

```

Val Leu Lys Thr Leu Ser Ile Arg Leu Val Ile Leu Leu Asn Cys Ser
1      5      10      15
Leu Ala Thr Asn Ala Cys Ser Gly Val Gln Lys Leu Arg Asp Glu Ser
      20      25      30
His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr Lys Leu Lys Asn Met
      35      40      45
Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile Gly Glu Ala Ser Val
      50      55      60
Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu Ala Ile Glu Lys Ala
      65      70      75      80
Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys Arg Lys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762

```

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu
1      5      10      15
Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln
      20      25      30
Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met
      35      40      45
Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu
      50      55      60
Glu Ile Lys Ala Leu Lys Gln Glu Gln

```

65

70

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763

```

Val Ile Phe Ile Ala Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro
1           5           10           15
Leu Arg Asp Arg Met Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser
20          25          30
Glu Lys Glu Glu Ile Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu
35          40          45
Lys His Ala Leu Lys Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu
50          55          60
Lys Leu Ile Ile Glu Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu
65          70          75          80
Arg Arg Gln Ile Ala Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu
85          90          95
Glu Asp Asn Pro His Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys
100         105         110
Asp Lys Lys Gly Gly Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys
115         120         125
Asp Phe Cys Val Ser Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu
130         135         140
Arg Met Val Phe Glu Ile Unk Pro Ile Asp Glu Glu Asn Lys Ile Gly
145         150         155         160
Ile Val Asn Gly Leu Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys
165         170         175
Ile Glu Ala Val Lys Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly
180         185         190
Ser Leu Gly Asp Val Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val
195         200         205
Val Lys Val Leu Leu Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro
210         215         220
Ser Glu Thr Asp Ala Glu Asn Unk Lys Lys Lys Val Leu Lys Val
225         230         235         240
Unk Asn Ala Tyr Asp Leu His Leu His Val Pro Lys Gly Leu Arg Leu
245         250         255
Lys Thr Ala Arg Ala Leu Gly Ser Leu Trp Arg Ala
260         265

```

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

634

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

```

Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1      5      10      15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
      20      25      30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
      35      40      45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
      50      55      60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
      65      70      75      80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
      85      90      95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
      100      105      110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
      115      120      125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
      130      135      140
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
      145      150      155      160
Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
      165      170      175
Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
      180      185      190
Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
      195      200      205
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
      210      215      220
Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
      225      230      235      240
Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
      245      250      255
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
      260      265      270
Phe

```

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

635

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

```

Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1      5      10      15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
      20      25      30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
      35      40      45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
      50      55      60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
      65      70      75      80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
      85      90      95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
      100      105      110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
      115      120      125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
      130      135      140
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
      145      150      155      160
Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
      165      170      175
Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
      180      185      190
Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
      195      200      205
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
      210      215      220
Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
      225      230      235      240
Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
      245      250      255
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
      260      265      270
Phe

```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

SUBSTITUTE SHEET (RULE 26)

636

```

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1      5      10      15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
      20      25      30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
      35      40      45
Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
      50      55      60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk
65      70      75      80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
      85      90      95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
      100     105     110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
      115     120     125
Leu Ile Thr Ser Pro
      130

```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

```

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1      5      10      15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
      20      25      30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
      35      40      45
Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
      50      55      60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk
65      70      75      80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
      85      90      95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
      100     105     110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
      115     120     125
Leu Ile Thr Ser Pro
      130

```

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

637

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766

```

Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1          5          10          15
Asn Pro Leu Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
          20          25          30
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
          35          40          45
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
          50          55          60
Ile Arg Ser Leu Leu Lys Pro
65          70

```

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766

```

Met Pro Pro Thr Unk Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1          5          10          15
Asn Pro Leu Unk Unk Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
          20          25          30
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
          35          40          45
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
          50          55          60
Ile Arg Ser Leu Leu Lys Pro
65          70

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

638

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767

```

Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met
1           5           10           15
Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys Ala Met Asn
20          25          30
Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn Gln Gln Pro
35          40          45
Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His Val Thr Pro
50          55          60
Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro Gln Asn His
65          70          75          80
His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser Asp Asn Leu
85          90          95
Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln
100         105         110
Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Glu
115         120         125
Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp
130         135         140
Leu Lys Gly
145

```

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768

```

Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn Ala Tyr Ser
1           5           10           15
Tyr Asn Ser Asp Ser Leu Phe Leu Tyr Asp Phe Ser Arg Pro Phe Ile
20          25          30
Lys Asn Ser Gly Ala Ile Leu Asp Ile Gly Ser Gly Cys Gly Val Leu
35          40          45
Gly Leu Leu Cys Ala Arg Asp Asn Pro Leu Ala Ser Val His Leu Val
50          55          60
Glu Lys Asp Ser Lys Met Ala Phe Cys Ser Gln Lys Asn Ala Leu Lys

```

SUBSTITUTE SHEET (RULE 26)

639

```

65          70          75          80
Phe Pro Asn Ala Gln Val Phe Glu Ser Asp Phe Leu Asp Phe Asn Pro
          85          90          95
Pro Ile Leu Tyr Asp Ala Ile Val Cys Asn Pro Pro Phe Tyr Ala Leu
          100         105         110
Gly Ser Ile Lys Ser Gln Ile Lys Gly His Ala Arg His Gln Ser Glu
          115         120         125
Leu Asp Phe Ala Ser Leu Val Ala Lys Val Lys Lys Cys Leu Lys Pro
          130         135         140

```

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769

```

Met Leu Ser Ala Leu Val Met Leu Pro Phe Met Glu Val Phe Tyr Tyr
1          5          10          15
Phe Asn Phe Pro Leu Trp Leu Asn Leu Phe Leu Gly Gln Thr Ile Gly
          20          25          30
Ala Val Ile Phe Phe Lys Leu Asp Lys Leu Ile Phe Ser Lys Lys
          35          40          45

```

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770

```

Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr
1          5          10          15
Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu Ile Lys Gln
          20          25          30
Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Unk Pro
          35          40          45

```

SUBSTITUTE SHEET (RULE 26)

640

```

Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Glu
  50          55          60
Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser
  65          70          75          80
Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr
          85          90          95
Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu
          100          105          110
Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu
          115          120          125
Leu

```

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771

```

Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn Asp Phe Leu
  1          5          10          15
Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu Leu Ser Leu
          20          25          30
Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser Ile Val Asn
          35          40          45
Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr Ala His Ser
          50          55          60
Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys Ala Leu Val
          65          70          75          80
Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu Val Ile Asn
          85          90          95
Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser Tyr Leu His
          100          105          110
Gln Lys Tyr Tyr Pro His Val Val Leu Glu Glu Phe Gly Ser Ile Leu
          115          120          125
Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met Leu Leu Phe
          130          135          140
Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile Gly Val Phe
          145          150          155          160
Gly Val Phe Phe Ser Ile Val Pro His Phe His Phe Phe Lys Asn Thr
          165          170          175
Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln Ser Tyr Gln
          180          185          190
Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe Ser Phe Phe
          195          200          205
Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe Ala Thr Leu
          210          215          220
Leu Gln Thr Leu Lys Leu Thr His Tyr Ile Phe Ile Phe Lys Glu Lys
          225          230          235          240
Glu Cys

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772

```

Met Gln Tyr Ala Asn Ala Tyr Gln Ala Tyr Gln His Asn Arg Val Ser
1          5          10          15
Val Glu Ser Pro Ala Lys Leu Ile Glu Met Leu Tyr Glu Gly Ile Leu
          20          25          30
Arg Phe Ser Ser Gln Ala Lys Arg Cys Ile Glu Asn Glu Asp Ile Glu
          35          40          45
Lys Lys Ile Tyr Tyr Ile Asn Arg Val Thr Asp Ile Phe Thr Glu Leu
          50          55          60
Leu Asn Ile Leu Asp Tyr Glu Lys Gly Gly Unk Val Ala Val Tyr Leu
65          70          75          80
Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln Ala Asn Val
          85          90          95
Glu

```

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773

```

Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Glu Thr Ala Pro Leu
1          5          10          15
Leu Thr Ser Leu Leu Ala Gly Ile Leu Thr Phe Leu Ser Pro Cys Val
          20          25          30
Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln Ile Ser Leu
          35          40          45

```

642

```

Glu Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val Phe Leu Lys
 50      55      60
Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu Gly Val Gly
 65      70      75      80
Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser Trp Val Asn
      85      90      95
Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His Phe Leu Gly
      100      105      110
Val Phe Arg Phe Ala Phe Leu Tyr Lys Thr Gln Ser Val Gly Leu Ala
      115      120      125
Ser Lys Ser Asn Ser Met Gln Arg Phe Thr Pro Phe Phe Leu Ala
 130      135      140

```

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774

```

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
 1      5      10      15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
      20      25      30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
      35      40      45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
      50      55      60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
      65      70      75      80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
      85      90      95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
      100      105      110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
      115      120      125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
      130      135      140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
      145      150      155      160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
      165      170      175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
      180      185      190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
      195      200      205
Asn His Asn Gln Phe Phe Ile Lys Asn
      210      215

```

(2) INFORMATION FOR SEQ ID NO:774:

SUBSTITUTE SHEET (RULE 26)

643

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774

```

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1      5      10      15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
20      25      30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
35      40      45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
50      55      60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65      70      75      80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
85      90      95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
100     105     110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
115     120     125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
130     135     140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145     150     155     160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
165     170     175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
180     185     190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
195     200     205
Asn His Asn Gln Phe Phe Ile Lys Asn
210     215

```

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

644

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775

```

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala
1          5          10          15
Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val
          20          25          30
Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu
          35          40          45
His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu
          50          55          60
Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val
65          70          75          80
Leu Lys Lys Gly

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

```

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1          5          10          15
Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
          20          25          30
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
          35          40          45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
          50          55          60
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

645

(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

```

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1      5      10      15
Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
      20      25      30
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
      35      40      45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
      50      55      60
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777

```

Met Arg Ile Leu Ile Leu Lys Asn Lys Pro Pro Thr Leu Arg Ser Lys
1      5      10      15
Ala Leu Thr Arg Ser Trp Gly Ile Asn Phe Ser Leu Lys Asn Thr Leu
      20      25      30
Ala Tyr Ala Phe Met Gly Phe Phe Asp Tyr Ala His Ala Asn Ser Ile
      35      40      45
Lys Leu Lys Asn Pro Asn Tyr Asn Ser Glu Ala Ala Gln Val Ala Ser
      50      55      60
Gln Ile Leu Gly Lys Gln Glu Ile Asn Arg Leu Thr Asn Ile Ala Asp
      65      70      75      80
Pro Arg Thr Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp
      85      90      95
Val Met Val Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe
      100      105      110
Gly Gly Ile Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Unk Pro Ser
      115      120      125
Phe Glu Gly Ile Leu Gly Glu Gln Ala Leu Val Ser Arg Lys Pro Leu
      130      135      140
Leu Ser Asn Phe Tyr Ser Met Trp Gly Leu Ala
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

646

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778

```

Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1      5      10      15
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
20      25      30
Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys
35      40      45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
50      55      60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65      70      75      80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
85      90      95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
100     105     110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
115     120     125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
130     135     140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Unk Lys Ile
145     150     155     160
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Lys Asn Unk Asn Unk
165     170     175
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk
180     185     190

```

(2) INFORMATION FOR SEQ ID NO:778:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778

```

Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1      5      10      15
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
20      25      30
Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys

```

SUBSTITUTE SHEET (RULE 26)

647

```

      35              40              45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
 50              55              60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
 65              70              75              80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
      85              90              95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
      100              105              110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
      115              120              125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser
 130              135              140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Unk Lys Ile
 145              150              155              160
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Unk Lys Asn Unk Asn Unk
      165              170              175
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk
      180              185              190

```

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779

```

Met Asn Val Lys Lys Lys Glu Lys Pro Gln Ser Gly Lys Ile Asp Arg
 1              5              10              15
Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr Phe Leu Ser
      20              25              30
Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro Ile Pro Gly
      35              40              45
Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met Ser Lys Thr
      50              55              60
Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys Leu Ala Arg
 65              70              75              80
Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Gln
      85              90              95
Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu Arg Tyr Phe
      100              105              110
His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu Leu Glu Arg
      115              120              125
Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val Asn Asn Lys
 130              135              140
Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn Lys Gln Glu
 145              150              155              160
Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly
      165              170

```

SUBSTITUTE SHEET (RULE 26)

648

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780

```

Met Trp Pro Unk Lys Leu Phe Leu Lys Pro Leu Lys Glu Thr Ser Leu
1          5          10          15
Ala Leu Val Gly Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala
20          25          30
Gly Leu Lys Arg Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Phe Leu
35          40          45
Ile Lys Arg Tyr Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile
50          55          60
Thr Ala Leu Leu Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu
65          70          75          80
Ile Val Ala Met Ala Ile Met Asn Gly Met Ser Lys Glu Phe Glu Lys
85          90          95
Lys Leu Phe Val Met Asn Tyr Pro Leu Thr Leu Tyr Thr Thr Ser Pro
100         105         110
Tyr Gly Ile Ser Glu Glu Val Val Gln Ala Leu Glu Lys Lys Phe Pro
115         120         125
Asn Leu Pro Phe Ser Unk Pro Ile Cys Lys Pro Lys Ala
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781

```

Met Val Ser Leu Leu Gly Ala Leu Lys Arg Thr Pro Cys Thr Asn Arg
1          5          10          15
Phe Tyr Leu Lys Ala Leu Leu Phe Ala Ile Phe Tyr His Ala Val Asn
20          25          30
Asn Phe Leu Thr Gln Cys Pro Pro His Gln Val Arg Glu Phe Phe Ser

```

SUBSTITUTE SHEET (RULE 26)

649

```

      35              40              45
Ser Arg His Ala Gln Gly Trp Lys Arg Glu Thr Leu Pro Cys Ala Leu
  50              55              60
Ser Phe Gln Asn Ala Leu
  65              70

```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782

```

Val His His Leu Unk Arg Leu Leu Asp Ser Gly Ser Glu Arg Cys Ile
 1              5              10              15
Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr Ser Asn Cys Ile Arg Ile
 20              25              30
Ile Thr His Lys Gly Glu Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr
 35              40              45
Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Glu Val Cys
 50              55              60
Pro Glu Leu Ala Ile Val Met Gly Asn Arg Phe Glu Asn Ala Ser Thr
 65              70              75              80
Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu Phe Leu Thr Ser Glu Gln
 85              90              95
Asp Ala Lys Asn Cys Ser His Ala Glu Phe Leu Gly Phe Gly Ala Val
100              105              110
Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala Thr Pro Leu Asp Tyr Val
115              120              125
Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu Glu Phe Unk Thr Ser Pro
130              135              140
Glu Ser His Lys Gly Asp Glu Asn Val
145              150

```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

650

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783

```

Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met Trp
1      5      10      15
Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly Phe
20      25      30
Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg Phe
35      40      45
Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp Trp
50      55      60
Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp Thr
65      70      75      80
Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu Ser
85      90      95
Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg Ile
100     105     110
Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu Ile
115     120     125
Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile Leu
130     135     140
Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr Arg
145     150     155     160
Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser
165     170     175
Glu Arg Lys Gly Leu Lys Leu
180

```

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784

```

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe
1      5      10      15
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Ser Leu Ile Leu
20      25      30
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu
35      40      45
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn
50      55      60
Leu Leu Val
65

```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

651

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

```

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1      5      10      15
Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp
20     25     30
Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys
35     40     45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu
50     55     60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu
65     70     75     80
Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
85     90     95
Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu Gln Asn Met
100    105    110
Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu
115    120    125
Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu
130    135    140
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
145    150    155    160
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
165    170    175
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
180    185    190
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
195    200    205
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
210    215    220
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
225    230    235    240
Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
245    250

```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

652

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

```

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1          5          10          15
Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp
          20          25          30
Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys
          35          40          45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu
          50          55          60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu
65          70          75          80
Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
          85          90          95
Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu Gln Asn Met
          100          105          110
Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu
          115          120          125
Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu
130          135          140
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
145          150          155          160
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
          165          170          175
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
          180          185          190
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
          195          200          205
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
210          215          220
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
225          230          235          240
Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
          245          250

```

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786

```

Val Phe Leu Val Gln Ser Trp Ala Leu Ser Leu Lys Ile Asp Ser Leu
1          5          10          15
Phe Ser Leu Phe Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro
          20          25          30
Phe Ala Leu Arg Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His

```

SUBSTITUTE SHEET (RULE 26)

653

```

      35          40          45
Tyr Gly Leu Glu Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu
  50          55          60
Lys Val Gly Val Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe
  65          70          75          80
Leu Leu Glu Arg Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile
      85          90          95
Arg Ser Val Leu Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln
      100          105          110
Lys Val Lys Ala Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln
      115          120          125
Lys Lys Glu Leu Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn
      130          135          140
Lys Asp Arg Asn Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe
      145          150          155          160
Lys Glu Leu Gln Glu His Ala Leu Phe Glu Ala Phe Asn
      165          170

```

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787

```

Met Ser Leu Ala Pro Ser Val Met Ala Gly Phe Leu Phe Cys Ala Gly
  1          5          10          15
Ser Cys Ser Leu Arg Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp
      20          25          30
Val Asp Thr Val Phe Leu Gly Asp Val Ala Ser Ala Tyr Phe Ala Leu
      35          40          45
Asp Asn Glu Pro Thr Lys Leu Leu Gly Met Val Arg Asp Thr Phe Ser
      50          55          60
His Leu Pro Phe Glu Ala Phe Cys Asp Phe Cys Glu Arg Thr Cys Lys
      65          70          75          80
Asn Phe Lys Ile Asp Leu Leu Arg Phe Ser Gln Asn Glu Leu Lys Arg
      85          90          95
Ile His Gln Gly Phe Asn Met Gly Phe Leu Val Ala Asn Leu Asp Leu
      100          105          110
Trp Arg Glu Asn Gly Phe Glu Lys Ile Ala Leu Glu Phe Leu Lys Thr
      115          120          125
Arg Gly Lys Asp Leu Phe Tyr Pro Glu Gln Cys Leu Ile Asn Met Val
      130          135          140
Phe Leu Glu Arg Ile Leu Glu Leu Pro Ile His Tyr Asn Cys Tyr Ser
      145          150          155          160
Asp Phe Phe Lys Glu His Tyr Pro Lys Ser Ile Ile Met Leu His Phe
      165          170          175
Ile Lys Tyr Lys Pro Trp Arg Ser Val Ser Ser Leu Asn Gly Arg Leu
      180          185          190
Ile Cys Tyr Glu Ala Glu Ala Ser Phe Trp Leu Ala Asn Leu Phe Cys
      195          200          205

```

SUBSTITUTE SHEET (RULE 26)

654

```

Thr Pro. Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys
    210                215                220
Asp Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile
225                230                235                240
Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe
    245                250                255
Glu Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

```

Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile
1          5          10          15
Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys
    20          25          30
Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly
    35          40          45
His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp
    50          55          60
Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser
    65          70          75          80
Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
    85          90          95
Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
    100         105         110
Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu
    115         120         125
Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu
    130         135         140
Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser
    145         150         155         160
Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
    165         170         175
Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr
    180         185         190
Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val
    195         200         205
Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro
    210         215         220
Phe Ile Leu Ala Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
    225         230         235         240
Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
    245         250         255
Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
    260         265         270
Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser

```

SUBSTITUTE SHEET (RULE 26)

655

275 280 285
 Leu Pro Lys Leu Val
 290

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile
 1 5 10 15
 Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys
 20 25 30
 Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly
 35 40 45
 His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp
 50 55 60
 Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser
 65 70 75 80
 Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
 85 90 95
 Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
 100 105 110
 Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu
 115 120 125
 Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu
 130 135 140
 Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser
 145 150 155 160
 Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
 165 170 175
 Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr
 180 185 190
 Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val
 195 200 205
 Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro
 210 215 220
 Phe Ile Leu Ala Ser Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
 225 230 235 240
 Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
 245 250 255
 Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
 260 265 270
 Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser
 275 280 285
 Leu Pro Lys Leu Val
 290

SUBSTITUTE SHEET (RULE 26)

656

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789

```

Val Ile Val Cys Ser Ala Ala Gly Leu Ser His Phe Phe Gly Phe Ser
1           5           10           15
Met Ser Leu Gly Ala Phe Ile Val Gly Met Ala Ile Ser Lys Ser Arg
20           25           30
Tyr Lys Ile Asn Val Gln Glu Glu Phe Ala Gln Leu Lys Asn Leu Phe
35           40           45
Leu Ala Leu Phe Phe Ile Thr Ile Gly Met Gln Ile Asn Val Ser Phe
50           55           60
Phe Met Glu Lys Phe Phe Val Val Ile Phe Leu Leu Ile Leu Val Met
65           70           75           80
Ser Phe Lys Thr Phe Ile Ile Tyr Ala Leu Leu Arg Phe Phe Arg Asp
85           90           95
Ala Lys Thr Ala Ile Lys Thr Ala Leu Ser Leu Ala Gln Ile Gly Glu
100          105          110
Phe Ser Phe Val Ile Phe Leu Asn Ser Gly Ser His Gln Leu Phe Asn
115          120          125
Leu Gln Glu Lys Lys Gly Ile Leu Gly Phe Leu His Gln Lys Asn Ile
130          135          140
Leu Asn Ile Ala Gln Asn Asp Ile His Gln Leu Leu Ile Leu Met Val
145          150          155          160
Val Phe Ser Met Leu Ala Thr Pro Phe Ile Leu Lys Tyr Leu Glu Ser
165          170          175
Ile Ala Gln Phe Ile Leu His Gln Lys Ser Gln Glu Asn Glu Pro Ala
180          185          190
Lys Lys

```

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...132

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790

```

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val
1      5      10      15
Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala
20      25      30
Leu Arg His Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn
35      40      45
Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe
50      55      60
Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg
65      70      75      80
Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn
85      90      95
Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly
100     105     110
Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys
115     120     125
Asn Gly Cys Phe
130

```

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791

```

Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Glu Lys Pro Leu Tyr
1      5      10      15
Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Met Glu Ile Leu
20      25      30
Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr
35      40      45
Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu His Gln Asp
50      55      60
Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg Arg Leu Lys
65      70      75      80
Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
85      90      95
Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln Glu Ile Asn
100     105     110
His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu Lys Gln Gly
115     120     125
Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Leu Ser Ile Ala Arg
130     135     140
Val Leu Ser Lys Lys Pro Gln Ile Ile Ile Ala Asp Glu Pro Thr Gly
145     150     155     160
Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met Leu Gln Asn
165     170     175

```

SUBSTITUTE SHEET (RULE 26)

658

Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr His Asp Glu
 180 185 190
 His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu Lys Glu Ser
 195 200 205
 Leu Ile Lys Glu Lys
 210

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792

Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Leu Phe Phe Gly Leu Asn
 1 5 10 15
 Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe
 20 25 30
 Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp Gln Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
 1 5 10 15
 Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
 20 25 30
 Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
 35 40 45
 Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
 50 55 60
 Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro

SUBSTITUTE SHEET (RULE 26)

659

```

65          70          75          80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
      85          90          95
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
      100         105         110
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
      115         120         125
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
      130         135         140

```

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

```

Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
1          5          10          15
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
      20         25         30
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
      35         40         45
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
      50         55         60
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro
65          70          75          80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
      85          90          95
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
      100         105         110
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
      115         120         125
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
      130         135         140

```

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

660

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794

```

Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu
 1             5             10             15
Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu
          20          25          30
Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Glu Ala Gln
      35          40          45
Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His
 50          55          60
Trp Asp Ser Thr Phe
65

```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

```

Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
 1             5             10             15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
          20          25          30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
      35          40          45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
 50          55          60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Unk Gln His Leu Arg
65          70          75          80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
      85          90          95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
      100          105          110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
      115          120          125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

661

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

```

Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1      5      10      15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
      20      25      30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
      35      40      45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
      50      55      60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Unk Gln His Leu Arg
      65      70      75      80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
      85      90      95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
      100      105      110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
      115      120      125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796

```

Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala Asn Leu Leu
1      5      10      15
Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr Phe Asp Glu
      20      25      30
Glu Ser Leu Lys Thr Thr Asp Pro Arg Glu Phe Val Tyr Leu Ala Cys
      35      40      45
Lys Gly Lys Leu Glu Lys Ala Lys Glu Leu Leu Ala Asn Asn Cys Ala
      50      55      60
Ile Val Val Ala Asp Ser Val Val Ser Val Gly Asn Arg Met Gln Arg
      65      70      75      80
Lys Ala Lys Asn Lys Arg Glu Ala Leu Glu Phe Leu Lys Arg Gln Asn
      85      90      95

```

SUBSTITUTE SHEET (RULE 26)

662

```

Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile Ser Pro Val
      100      105      110
Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu Lys Ala Phe
      115      120      125
Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu Trp Gln Gly
      130      135      140
Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro Tyr Ile Lys
      145      150      155      160
Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn Val Glu Gly
      165      170      175
Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu Leu
      180      185      190

```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797

```

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
1      5      10      15
Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys
      20      25      30
Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
      35      40      45
Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr
      50      55      60
Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
      65      70      75      80
Arg Tyr Gly

```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797

```

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
1          5          10          15
Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys
20          25          30
Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
35          40          45
Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr
50          55          60
Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
65          70          75          80
Arg Tyr Gly

```

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798

```

Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg Phe Val Phe
1          5          10          15
Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn Asp Ile Val
20          25          30
Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln Tyr Cys Cys
35          40          45
Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His Lys Ile Glu
50          55          60
Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu Tyr Cys Ile
65          70          75          80
Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His Ala Thr Asn
85          90          95
Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe Asn Asp Thr
100          105          110
Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly Val Ile Ser
115          120          125
Lys Asp Ser Leu Leu Leu Lys
130          135

```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

664

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799

```

Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Gly Cys Val Gly
1      5      10      15
Ser Thr Val Ala Lys Ile Leu Gln Glu Asn Gln Glu Ile Ile Lys Asp
20      25      30
Arg Ala Gly Val Glu Ile Lys Ile Lys Lys Ala Val Val Arg Asp Val
35      40      45
Lys Lys His Lys Gly Tyr Ala Phe Glu Ile Ser Asp Asp Leu Glu Ser
50      55      60
Val Ile Glu Asp Lys Gly Ile Asp Ile Val Val Glu Leu Met Gly Gly
65      70      75      80
Val Glu Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala Lys Gln Lys
85      90      95
Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His Arg Tyr Glu
100     105     110
Leu Glu Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Glu Ala Ser Val
115     120     125
Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly Leu Ser Ala
130     135     140
Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr Ser Asn Tyr
145     150     155     160
Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys Asp Ala Leu
165     170     175
Lys Asp Ala Gln His Leu Gly Tyr Ala Glu Leu Asn Pro Glu Phe Asp
180     185     190
Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu Ala Ser Leu
195     200     205
Ala Tyr Gly Ile Asp Ala Lys Leu Glu Glu Ile Leu Ile Glu Gly Ile
210     215     220
Glu Lys Ile Glu Pro Asp Asp Met Glu Phe Ala Lys Glu Phe Gly Tyr
225     230     235     240
Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gly Leu His
245     250     255

```

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800

SUBSTITUTE SHEET (RULE 26)

```

Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile Ala Ser Trp
1      5      10      15
Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe Ser Lys Ile
20      25      30
Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala Leu Leu Asp
35      40      45
Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn Leu Cys Ala
50      55      60
Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp Asp Val Ile
65      70      75      80
Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn Ala Leu Phe
85      90      95
Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr Ser Lys Ala
100     105     110
Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln Ala Leu Ser
115     120     125
Asn Ala Val Leu Arg Leu Ser Arg Gly Glu Ile Glu Asp Val Phe Val
130     135     140
Gly Glu Cys Phe Asn Ser Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu
145     150     155     160
Asp Lys Thr Ala His Phe Ile Glu Ala Ser Leu Lys Ser Met Ala Ile
165     170     175
Leu Leu Asn Lys Asp Ala Lys Met Tyr Ala Asp Phe Gly Leu His Phe
180     185     190
Gly Met Ala Phe Gln Ile Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp
195     200     205
Ala Asn Thr Leu Gly Lys Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys
210     215     220
Thr Thr Leu Pro Tyr Leu Leu Leu Tyr Glu Lys Leu Asn Gln His Glu
225     230     235     240
Gln Gly Phe

```

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801

```

Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val
1      5      10      15
Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn
20      25      30
Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu Asn Val Ala
35      40      45
Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys Thr Asp Ile
50      55      60
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys
65      70      75      80

```

SUBSTITUTE SHEET (RULE 26)

666

```

Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser
      85          90          95
Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser
      100        105        110
Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe
      115        120        125
Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val
      130        135        140
Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu
      145        150        155        160
Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe Ile Thr Ile
      165        170        175
Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys
      180        185        190
Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu
      195        200        205
Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile
      210        215        220
Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile
      225        230        235        240
Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
      245        250

```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802

```

Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser Lys Arg Ile
1      5      10      15
Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met Leu Ala Tyr
      20      25      30
Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys Val Phe Ile
      35      40      45
Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn Tyr Gly Ala
      50      55      60
Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Asp Arg Ala Thr
      65      70      75      80
Thr Leu Glu Val Met Ala Tyr His Met Lys Glu Leu Glu Leu Lys Asp
      85      90      95
Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val Ser Val Phe Leu Gln Glu
      100     105     110
Lys His Leu Gln Asn Ala Phe Glu Thr Leu Lys Gln Asn Gln Asn Thr
      115     120     125
Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser Ala Ser Pro Ile Val Leu
      130     135     140
Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu Leu Lys Ser Ile Gln Thr
      145     150     155     160
Arg Ala Arg Lys Ile

```

SUBSTITUTE SHEET (RULE 26)

165

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803

```

Met Ser Asn Gln Ala Ser His Leu Asp Asn Phe Met Asn Ala Lys Asn
1      5      10      15
Pro Lys Ser Phe Asp Asn Lys Gly Asn Thr Lys Phe Ile Ala Ile
20     25     30
Thr Ser Gly Lys Gly Gly Val Gly Lys Ser Asn Ile Ser Ala Asn Leu
35     40     45
Ala Tyr Ser Leu Tyr Lys Lys Gly Tyr Lys Val Gly Val Phe Asp Ala
50     55     60
Asn Ile Gly Leu Ala Asn Leu Asp Val Ile Phe Gly Val Lys Thr Gln
65     70     75     80
Lys Asn Ile Leu His Asp Leu Lys Gly Glu Asp Lys Leu Lys Glu Ile
85     90     95
Ile Cys Glu Ile Glu Pro Gly Leu Cys Leu Ile Pro Gly Asp Ser Gly
100    105    110
Glu Glu Ile Leu Lys Tyr Ile Ser Glu Ala Glu Asp Phe Asp Ser Phe
115    120    125
Leu Asp Glu Glu Gly Val Leu Ser Ala Leu Ile Tyr Ile Leu Ile Asn
130    135    140
Thr Phe Ser Lys Asn Leu Gly Pro Leu Ser Gln Thr Phe Leu Asn Phe
145    150    155    160
Gln Ser Phe Leu Phe Ile Phe Ile Gln Ser Pro
165    170

```

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

SUBSTITUTE SHEET (RULE 26)

668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804

```

Met Gln His Leu Val Leu Ile Gly Phe Met Gly Ser Gly Lys Ser Ser
1      5      10      15
Leu Ala Gln Glu Leu Gly Leu Ala Leu Lys Leu Glu Val Leu Asp Thr
20      25      30
Asp Met Ile Ile Ser Glu Arg Val Gly Leu Ser Val Arg Gly Ile Phe
35      40      45
Glu Glu Leu Gly Glu Asp Asn Phe Arg Met Phe Glu Lys Ile
50      55      60

```

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805

```

Met Ser Ile Lys Glu Asn Leu Glu Gln Val Arg Asn Glu Phe Lys Ser
1      5      10      15
Asp Glu Lys Leu Leu Glu Gly Ala Phe Arg Leu Glu Lys Phe Phe Lys
20      25      30
Arg Tyr Lys Trp Val Leu Leu Phe Ile Val Val Ala Phe Ile Ala Tyr
35      40      45
Leu Gly Asp Thr Lys Leu Gln Asp Tyr Lys His Glu Gln Thr Arg Glu
50      55      60
Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn Ile
65      70      75      80
Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp Leu
85      90      95
Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe Lys
100      105      110
Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys Tyr
115      120      125
Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser Pro
130      135      140
Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr Glu
145      150      155      160
Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser Thr
165      170      175
Ile Pro Leu Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys His
180      185      190
Tyr Gly Met Leu Glu Asp Ile
195

```

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

669

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806

```

Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1          5          10          15
Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
20        25        30
Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
35        40        45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
50        55        60
Ala Lys Glu Lys His Val Lys Glu Asn Val Unk Pro Leu His Phe Cys
65        70        75        80
Unk Ala Gly His Ile Unk Val Val Pro Pro Gly Unk Unk Unk Unk
85        90        95
Asp Ser Phe Unk Unk Ile Ile Lys Glu Gly Phe Leu Tyr Gly Arg Gly
100       105       110
Ala Gln Asp Met Lys Gly Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
115       120       125
Lys Phe
130

```

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806

```

Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1          5          10          15
Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
20        25        30
Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
35        40        45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
50        55        60
Ala Lys Glu Lys His Val Lys Glu Asn Val Unk Pro Leu His Phe Cys
65        70        75        80

```

SUBSTITUTE SHEET (RULE 26)

670

```

Unk Ala Gly His Ile Unk Val Val Pro Pro Gly Unk Unk Unk Unk
      85          90          95
Asp Ser Phe Unk Unk Ile Ile Lys Glu Gly Phe Leu Tyr Gly Arg Gly
      100          105          110
Ala Gln Asp Met Lys Gly Gly Val Gly Unk Phe Unk Arg Cys Unk Unk
      115          120          125
Lys Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807

```

Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly Ala Ile Leu
1          5          10          15
Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Glu Glu Tyr Leu Lys
      20          25          30
Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Glu Gln Glu Ser Ser Ile
      35          40          45
His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala Met Gly Gly
      50          55          60
Gly Arg Met Gly Val Leu Glu Thr Ser Phe Lys Glu Glu Cys Glu Ser
      65          70          75          80
Asp Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Glu Val Asp
      85          90          95
Arg Lys Asn Gly Val
      100

```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808

SUBSTITUTE SHEET (RULE 26)

671

```

Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala Leu Ile Ile Ser Met
1      5      10      15
Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val Phe Leu Gly Ala Gly
20      25      30
Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys
35      40      45
Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr
50      55      60
Gln Phe Phe Phe Glu Lys His Phe Gly Leu Arg Leu Tyr Gly Val Phe
65      70      75      80

```

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809

```

Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe Leu Ile Ile
1      5      10      15
Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val Thr Thr Asp
20      25      30
Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val Ala Ser Gln
35      40      45
Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr Asp Lys Glu
50      55      60
Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg Phe Val Glu
65      70      75      80
Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His Gly Gly Ile
85      90      95
Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala Lys Ser Gly
100     105     110
Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu Val Lys Asn
115     120     125
Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu Lys Glu Ala
130     135     140
Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu Glu Ile Leu
145     150     155     160
Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr Tyr Gly Val
165     170     175
Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp Lys Leu Thr
180     185     190
Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala Pro Ser Phe
195     200     205
Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg Ala Asn Asp
210     215     220
Ile Leu Arg Arg Leu Tyr Ser Leu Gly Unk Ile Ser Ser Asn Glu Leu
225     230     235     240
Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln Thr Ser Thr
245     250     255

```

SUBSTITUTE SHEET (RULE 26)

672

Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys Gln Leu Asp
 260 265 270
 Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys Leu Thr Ile
 275 280 285
 Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg Phe Gly His
 290 295 300
 Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys Thr Asn Ala
 305 310 315 320
 Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Ser Met Ile Val Thr
 325 330 335
 Glu Thr Ser Thr Gly Lys Ile Leu Ala Leu Val Gly Gly Ile Asp Tyr
 340 345 350
 Lys Lys Ser Ala Phe Asn Arg Ala Thr Gln Ala Lys Arg Gln Phe Gly
 355 360 365
 Ser Ala Ile Lys Pro Phe Val Tyr Gln Ile Ala Phe Asp Asn Gly Tyr
 370 375 380
 Ser Thr Thr Ser Lys Ile Pro Asp Thr Ala Arg Asn Phe Glu Asn Gly
 385 390 395 400
 Asn Tyr Ser Lys Asn Ser Val Gln Asn His Ala Trp His Pro Ser Asn
 405 410 415
 Tyr Unk Arg Lys Phe Leu Gly Leu Val Thr Leu Gln Glu Ala Leu Ser
 420 425 430
 His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ala Ile Ala Trp Leu
 435 440 445

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810

Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro
 1 5 10 15
 Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser
 20 25 30
 Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu
 35 40 45
 Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu
 50 55 60
 Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys
 65 70 75 80
 Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
 85 90 95
 Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
 100 105 110
 Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu
 115 120 125
 Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala
 130 135 140
 Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser

SUBSTITUTE SHEET (RULE 26)

673

```

145          150          155          160
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val
          165          170          175
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile
          180          185          190
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu
          195          200          205
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu
210          215

```

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811

```

Met Met Asp Lys Val Gly Phe Lys Ser Gln Gly Ile Phe Val Met Asp
1          5          10          15
Ala Ser Lys Arg Asp Gly Arg Leu Asn Ala Tyr Phe Gly Gly Leu Gly
20          25          30
Lys Asn Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly
35          40          45
Thr Glu Unk Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys
50          55          60
Asn Lys Asp Leu Leu Lys Asn Leu Gly Ile Met Gly Gly Leu Leu Ala
65          70          75          80
Leu Val Phe Ala Leu Ile Ala His Leu Pro Pro Leu Val Phe Glu Gly
85          90          95
Phe Asn Val Ser Gln Thr Pro Ala Ser Leu Ile Thr Ile Leu Leu Leu
100          105          110
Phe Leu Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe
115          120          125
Ser Arg Lys Asn Glu Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser
130          135          140
Ser Lys Glu Thr Leu Ala Lys Ala Leu Val Ser Ile Val Asn Glu Asn
145          150          155          160
Lys Ala Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr
165          170          175
His Pro Pro Leu Leu Glu Arg Leu Lys Ala Leu Asp Tyr Glu Ile Glu
180          185          190

```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

674

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

```

Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1      5      10      15
Thr Arg Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
      20      25      30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser
      35      40      45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile
      50      55      60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
      65      70      75      80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
      85      90      95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
      100     105     110
Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met
      115     120     125
Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
      130     135     140
Ala Arg Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
      145     150     155     160
Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
      165     170     175
Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
      180     185     190
Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
      195     200     205
Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
      210     215     220
Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
      225     230     235     240
Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
      245     250     255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
      260     265     270
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
      275     280     285
Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
      290     295     300
Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
      305     310     315     320
Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
      325     330     335
Lys Asn Phe Glu
      340

```

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

675

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

```

Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1      5      10      15
Thr Arg Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
      20      25      30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser
      35      40      45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile
      50      55      60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
      65      70      75      80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
      85      90      95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
      100     105     110
Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met
      115     120     125
Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
      130     135     140
Ala Arg Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
      145     150     155     160
Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
      165     170     175
Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
      180     185     190
Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
      195     200     205
Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
      210     215     220
Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
      225     230     235     240
Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
      245     250     255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
      260     265     270
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
      275     280     285
Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
      290     295     300
Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
      305     310     315     320
Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
      325     330     335
Lys Asn Phe Glu
      340

```

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

676

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813

```

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro
1      5      10      15
Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu
20     25     30
Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Leu Asp Lys Glu
35     40     45
Thr Asn Thr Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu
50     55     60
Leu Tyr Lys Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr
65     70     75     80
Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu
85     90     95
Asn Leu Lys Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe
100    105    110
Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg
115    120    125
Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser
130    135    140
Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp
145    150    155    160
Leu Lys Leu Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile
165    170    175
Glu Ile Asn Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser
180    185    190
Val Gly Asn Asp Ala Lys Ala His Ser
195    200

```

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814

```

Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val Gly Ala Asn
1      5      10      15
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn

```

SUBSTITUTE SHEET (RULE 26)

677

```

      20      25      30
Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu
      35      40      45
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val
      50      55      60
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys
      65      70      75      80
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu
      85      90      95
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile
      100      105      110
Tyr Tyr Thr Arg Val Arg Asn Gln Ser Lys Leu Val Phe Ala Gly Phe
      115      120      125
Lys Gly
      130

```

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815

```

Met Lys Ile Gln Thr Ile Ser Thr Leu Val Leu Thr Ile Ile Met Val
1      5      10      15
Ile Gln Lys Met Ile Val Gly Lys Ile Ser Pro His Lys Thr Ala Glu
      20      25      30
Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala Val Leu Asp Ser Gln
      35      40      45
Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe Glu Phe Thr Asn Ser
      50      55      60
Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys Val Asn Pro Gly Thr
      65      70      75      80
Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys Tyr Val Leu Asn Lys
      85      90      95
Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala Asp Leu Asp Val Ile
      100      105      110
Val Leu Lys Asp Ser Gly Val Val Gly Unk Unk Asn Gly Tyr Gly Asn
      115      120      125
Asp Gly Glu Tyr Gly Thr Leu Gly Val Unk Ala Tyr Ala Leu Gly Ser
      130      135      140

```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

678

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816

```

Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser Tyr
1      5      10      15
Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys Lys
      20      25      30
Glu Arg Phe Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro
      35      40      45
Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe
      50      55      60
Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met Lys
65      70      75      80
Leu Leu Ser Lys Lys Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val
      85      90      95
Thr Phe Ile Leu Ile Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr
      100      105      110
Leu Gly Val Gln Thr Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly
      115      120      125
Ile Ala Val Ala Leu Ala Leu Lys Asp Tyr Leu Ser Ser Ile Ala Gly
      130      135      140
Gly Ile Ile Leu Ile Ile Leu His Pro Phe Lys Lys Gly Asp Ile Ile
145      150      155      160
Glu Ile Ser Gly Leu Glu Gly Lys Val Glu Ala Leu Asn Phe Phe Asn
      165      170      175
Thr Ser Leu Arg Leu His Asp Gly Arg Leu Ala Val Leu Pro Asn Arg
      180      185      190
Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys Arg
      195      200      205
Arg Ile Glu Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu Leu
      210      215      220
Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Glu Lys Ile Asp
225      230      235      240
Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser
      245      250      255
Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe
      260      265      270
Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala
      275      280      285
Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys
      290      295      300
Gln Asp Ser Ser Lys
305

```

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

679

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817

```

Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Unk Leu Lys Lys Arg
1           5           10           15
His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe
20           25           30
Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr
35           40           45
Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn
50           55           60
Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu Phe Glu Met
65           70           75           80
Thr Thr Thr Val Ile Asn Ile Pro Thr Phe Ser Phe Lys Val Pro Thr
85           90           95
Thr Asn Gln Unk Leu Tyr Ser Val Thr Ser Leu Glu Ile Asp Lys Ser
100          105          110
Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Gly Asn Ile
115          120          125
Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala
130          135          140
Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val
145          150          155          160
Thr Leu Ala Ser
  
```

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818

```

Met Cys Leu Ala Ile Pro Ser Lys Val Ile Ala Ile Asn Asp Asn Val
1           5           10           15
Ala Leu Leu Glu Thr Leu Gly Val Gln Arg Glu Ala Ser Leu Asp Leu
20           25           30
Met Gly Glu Ser Val Lys Val Gly Asp Tyr Val Leu Leu His Ile Gly
35           40           45
Tyr Val Met Ser Lys Asp
50
  
```

(2) INFORMATION FOR SEQ ID NO:819:

SUBSTITUTE SHEET (RULE 26)

680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819

```

Met Lys Tyr Leu Trp Leu Phe Leu Ile Tyr Ala Ile Gly Leu Phe Ala
1      5      10      15
Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gln Lys Leu Pro Lys
      20      25      30
Ile Glu Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr Ala Leu Lys
      35      40      45
Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln His Phe Asp
      50      55      60
Val Ser Gln Asn Lys Glu Gln Gly Ala Ile Asn Tyr Ala Glu Leu Lys
65      70      75      80
Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala Val Glu Asn
      85      90      95
Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp Thr Gly Thr
      100     105     110
Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp Leu Tyr Pro
      115     120     125
Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr Leu Lys Ala
130     135     140
Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser Lys Tyr Ile
145     150     155     160
Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asn Tyr Thr Met Arg Tyr
      165     170     175
Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe Pro Lys Trp
      180     185     190
Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr
      195     200

```

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820

SUBSTITUTE SHEET (RULE 26)

681

```

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1      5      10      15
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu
      20      25      30
Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr
      35      40      45
Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg
      50      55      60
Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu
      65      70      75      80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys
      85      90      95
Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk
      100      105      110
Lys Thr Unk Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser
      115      120      125
Thr Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp
      130      135      140
Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile
      145      150      155      160
Leu Asn Met Ala Gly Leu Lys Trp
      165

```

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820

```

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1      5      10      15
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu
      20      25      30
Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr
      35      40      45
Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg
      50      55      60
Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu
      65      70      75      80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys
      85      90      95
Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk
      100      105      110
Lys Thr Unk Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser
      115      120      125
Thr Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp
      130      135      140
Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile
      145      150      155      160

```

SUBSTITUTE SHEET (RULE 26)

682

Leu Asn Met Ala Gly Leu Lys Trp
165

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821

```

Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe Val Pro Ile Leu
1          5          10          15
Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro Leu Ala Gln Ser
20          25          30
Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser Ile Thr Ile Ile
35          40          45
Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro His Ser Glu Thr
50          55          60
Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro Leu Leu Glu Phe
65          70          75          80
Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala Phe Val Phe Leu
85          90          95
Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys Asn Phe Met Pro
100         105         110
Ala Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu Thr Thr Pro Ser
115         120         125
Ile Ser Leu Asp Gln Ser Lys Asp Leu Met Leu Asn Ile Glu Ser Ala
130         135         140
Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val Ala Arg Thr Gly
145         150         155         160
Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn Gln Thr Asp Thr
165         170         175
Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp
180         185

```

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

683

(A) NAME/KEY: misc_feature
(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822

```

Val Gly Tyr Ile Pro Unk Glu Lys Ile Val Gly Ile Ser Ala Ile Ala
1           5           10           15
Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln Glu Arg Leu
20           25           30
Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu Pro Arg Gly
35           40           45
Val Ile Val Val Cys Glu Ala Lys Pro Leu Val His Glu His Ala Arg
50           55           60
Gly Ala Lys Ala Lys Cys Asp His
65           70

```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

```

Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
1           5           10           15
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
20           25           30
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val
35           40           45
Arg Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile
50           55           60
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65           70           75           80
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
85           90           95
Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu
100          105          110
Leu Gly Arg Unk Gln Thr Unk Asp Unk
115          120

```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

684

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

```

Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
1          5          10          15
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
          20          25          30
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val
          35          40          45
Arg Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile
          50          55          60
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65          70          75          80
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
          85          90          95
Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu
          100          105          110
Leu Gly Arg Unk Gln Thr Unk Asp Unk
          115          120

```

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824

```

Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys
1          5          10

```

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825

```

Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser Leu Gly Phe
1          5          10          15
Leu Lys Ala His Glu Val Ser Ala Glu Ile Ala Asp Ile Phe Tyr
          20          25          30
Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His Thr Lys Gly
          35          40          45
Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala Arg Glu Asp
          50          55          60
Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala Ser Val Arg
65          70          75          80
Tyr Ser Leu Gly Gly Val Val Asp Trp Thr Ile Lys Ala Arg Leu Gly
          85          90          95
Glu Trp Arg

```

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826

```

Val Ile Lys Pro His Ser Val Gly Leu Val Arg Ile Gly Ile Cys Leu
1          5          10          15
Ser Leu Glu Val Gly Tyr Glu Leu Gln Val Arg Thr Arg Ser Gly Leu
          20          25          30
Ala Leu Asn His Gln Val Met Val Leu Asn Unk Pro Gly Thr Val Asp
          35          40          45
Asn Asp Tyr Arg Gly Glu Ile Lys Val Ile Leu Ala Asn Leu Ser Asp
          50          55          60
Lys Asp Phe Lys Val Gln Val
65          70

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

686

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```

Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1           5           10           15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20           25           30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35           40           45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50           55           60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65           70           75           80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85           90           95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
100          105          110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
115          120          125
Unk Gly Ala Unk Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile
130          135          140
Leu Val Ala Leu Gly
145
  
```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```

Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1           5           10           15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20           25           30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35           40           45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50           55           60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65           70           75           80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85           90           95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
  
```

SUBSTITUTE SHEET (RULE 26)

687

```

      100      105      110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
      115      120      125
Unk Gly Ala Unk Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile
      130      135      140
Leu Val Ala Leu Gly
145

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828

```

Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu Phe Tyr Phe
1      5      10      15
Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn Pro Lys Thr
      20      25      30
Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu Leu Val Gln
      35      40      45
Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly Ala Tyr Met
50      55      60
Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu Asp Asn Ala
65      70      75      80
Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu Asn Ser Glu
      85      90      95
Gln Gln Asn Leu Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys
100      105      110
Glu Asn Phe Glu Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly
115      120      125
Glu Tyr Thr Lys Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala
130      135      140
Tyr Ala Asp Gly Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp
145      150      155      160
Val Gly Ala Phe Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr
165      170      175
Asp Asn Phe Glu His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu
180      185      190
Glu Ala Lys Asn Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp
195      200      205
Leu Glu Lys Lys Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met
210      215      220
Asn Asp Asn Lys Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys
225      230      235      240
Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
245      250      255

```

(2) INFORMATION FOR SEQ ID NO:829:

SUBSTITUTE SHEET (RULE 26)

688

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829

```

Met Glu Val Glu His Gly Lys Ile Glu Thr Thr Leu Ser Leu Gly Ala
1      5      10      15
Ser His Leu Glu Val Ile Lys Met Met Leu Leu Glu Ser Leu Pro Ser
      20      25      30
Leu Val Asn Asn Ile Thr Ile Thr Leu Ile Ser Leu Ile Gly Tyr Ser
      35      40      45
Ala Lys Ala Gly Ala Leu Gly Ala Gly Gly Leu Gly Asp Leu Ala Ile
      50      55      60
Arg Ile Gly Tyr Gln Ser Tyr Arg Gly Asp Val Leu Phe Tyr Ala Val
65      70      75      80
Val Val Ile Ile Val Leu Val Gln Ile Ile Gln Ser Ala Gly Asp Tyr
      85      90      95
Val Val Lys Arg Leu Arg Lys Asn Lys Tyr
      100      105

```

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830

```

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
1      5      10      15
Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
      20      25      30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
      35      40      45
Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
      50      55      60
Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
65      70      75      80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp

```

SUBSTITUTE SHEET (RULE 26)

				85					90					95		
Thr	Pro	Cys	Glu	Ile	Glu	Thr	Ile	Glu	Arg	Glu	Phe	Gly	Gln	Asp	Val	
			100					105					110			
Ala	Asn	Leu	Val	Asp	Ala	Leu	Thr	Lys	Ile	Thr	Glu	Ile	Arg	Lys	Glu	
		115					120					125				
Glu	Leu	Gly	Val	Ser	Ser	Gln	Asp	Pro	Arg	Met	Val	Val	Ser	Ala	Leu	
	130					135					140					
Thr	Phe	Arg	Lys	Ile	Leu	Ile	Ser	Ala	Ile	Gln	Asp	Pro	Arg	Ala	Leu	
145					150					155					160	
Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	Leu	Asp	Ala	
				165					170					175		
Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	Leu	Ala	Val	
			180					185					190			
Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	Glu	
		195					200					205				
Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	Tyr	Lys	Asn	
	210					215					220					
Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	Leu	Lys	Leu	
225					230					235					240	
Asn	Ala	Phe	Ala	Ser	Lys	Leu	Glu	Lys	Lys	Leu	Phe	Asp	Ser	Gly	Phe	
				245					250					255		
Ser	His	Ser	Asp	Phe	Lys	Leu	Val	Thr	Arg	Val	Lys	Arg	Pro	Tyr	Ser	
			260					265					270			
Ile	Tyr	Leu	Lys	Met	Gln	Arg	Lys	Gly	Ala	Val	Asn	Ile	Asp	Glu	Ile	
		275					280					285				
Leu	Asp	Leu	Leu	Ala	Ile	Arg	Ile	Leu	Leu	Lys	Asn	Pro	Ile	Asp	Cys	
	290					295					300					
Tyr	Lys	Val	Leu	Gly	Ile	Ile	His	Leu	Asn	Phe	Lys	Pro	Ile	Val	Ser	
305					310					315					320	
Arg	Phe	Lys	Asp	Tyr	Ile	Ala	Leu	Pro	Lys	Glu	Asn	Gly	Tyr	Lys	Thr	
				325					330					335		
Ile	His	Thr	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Val	Tyr	Glu	Val	Gln	Ile	
			340					345					350			
Arg	Thr	Phe	Asp	Met	His	Met	Gly	Ala	Glu	Tyr	Gly	Asn	Ser	Ala	His	
		355					360					365				
Trp	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Asp	His	Glu	Glu	His	His	Glu	Gly	
	370				375						380					
Met	Arg	Trp	Leu	Gln	Asn	Phe	Lys	Tyr	His	Asp	Ser	Asp	Leu	Lys	Asn	
385					390					395					400	
Asp	Pro	Lys	Glu	Phe	Tyr	Glu	Leu	Ala	Lys	Asn	Asp	Leu	Tyr	Arg	Glu	
				405					410					415		
Asp	Ile	Val	Val	Phe	Ser	Pro	His	Gly	Asp	Thr	Tyr	Thr	Leu	Pro	Val	
			420					4								

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

690

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831

```

Val Val Val Val Glu Asn Ile Lys Asp Ala Val Pro Leu Ala Gln Ser
1          5          10          15
Leu Ile Unk Gly Gly Ile Pro Ile Ile Glu Val Thr Leu Arg Ser Asn
20          25          30
Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala Lys Asn Val Pro Lys Met
35          40          45
Arg Val Gly Ala Gly Thr Ile Leu Asn Leu Thr Gln Leu Glu Gln Ala
50          55          60
Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser Pro Gly Leu Thr Ile Lys
65          70          75          80
Leu Leu Glu His Ala Lys Lys Lys Asp Met Pro Leu Ile Pro Gly Val
85          90          95
Ser Ser Ser Ser Glu Val Met Gln Ala Leu Glu Leu Gly Tyr Asn Ala
100         105         110
Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly Gly Arg
115         120

```

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832

```

Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp
1          5          10          15
Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly Thr Ser
20          25          30
Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr Lys Val
35          40          45
Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu Thr Ala
50          55          60
Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Phe Glu
65          70          75          80
Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn Gln Lys
85          90          95
Ile Ile Ile Asp Asp Asn Phe Asn Gly Asn Leu Lys Gly Met
100         105         110

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

```

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1      5      10      15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
20      25      30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
35      40      45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
50      55      60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65      70      75      80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
85      90      95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
100      105      110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
115      120      125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
130      135      140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145      150      155      160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
165      170      175
Ser Glu Arg Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
180      185      190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
195      200      205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
210      215      220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225      230      235      240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
245      250      255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
260      265      270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
275      280      285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
290      295      300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305      310      315      320
Gly Gly Phe His Phe
325

```

SUBSTITUTE SHEET (RULE 26)

692

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

```

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1           5           10           15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
20           25           30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
35           40           45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
50           55           60
Ala Asn Gln Ser Ile Glu Ala Leu Gln Asn Val Pro Gly Val His
65           70           75           80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
85           90           95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
100          105          110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
115          120          125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
130          135          140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145          150          155          160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
165          170          175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
180          185          190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
195          200          205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
210          215          220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225          230          235          240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
245          250          255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
260          265          270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
275          280          285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
290          295          300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305          310          315          320
Gly Gly Phe His Phe
325

```

(2) INFORMATION FOR SEQ ID NO:834:

SUBSTITUTE SHEET (RULE 26)

693

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

```

Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Glu Lys Gly
1           5           10           15
Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu Ser Glu Asp
      20           25           30
Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala Val Leu Gln
      35           40           45
Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly Ser Gly Asp
      50           55           60
Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val Gly Arg Phe
      65           70           75           80
Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro Met Cys Gln
      85           90           95
Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile Lys Ala Trp
      100          105          110
Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val Asp Cys Val
      115          120          125
Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu Asp Phe Glu
      130          135          140
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
      145          150          155          160
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
      165          170          175
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Unk
      180          185          190
Lys Unk Lys Unk Tyr Ile Unk Unk Leu Lys Unk Unk His Leu Unk Val
      195          200          205
Phe Asn Gln Ile Tyr Glu Ile Pro Thr Unk Thr Phe Leu Leu Glu Lys
      210          215          220
Unk Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
      225          230          235          240
Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
      245          250

```

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

694

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

```

Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Glu Lys Gly
1          5          10          15
Asn Ala Leu Asp Lys Arg Val Leu Glu Trp Leu Leu Ser Glu Asp
20          25          30
Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala Val Leu Gln
35          40          45
Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly Ser Gly Asp
50          55          60
Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val Gly Arg Phe
65          70          75          80
Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro Met Cys Gln
85          90          95
Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile Lys Ala Trp
100         105         110
Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val Asp Cys Val
115         120         125
Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu Asp Phe Glu
130         135         140
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
145         150         155         160
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Unk Gly
165         170         175
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Unk
180         185         190
Lys Unk Lys Unk Tyr Ile Unk Unk Leu Lys Unk Unk His Leu Unk Val
195         200         205
Phe Asn Gln Ile Tyr Glu Ile Pro Thr Unk Thr Phe Leu Leu Glu Lys
210         215         220
Unk Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
225         230         235         240
Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
245         250

```

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835

```

Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu Leu
1          5          10          15
Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu Arg

```

SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

696

```

Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser Lys
545          550          555          560
Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu
          565          570          575
Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr
          580          585          590
Asp Gly Arg Ser Phe
          595

```

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836

```

Val Asn Leu Gly Ala Tyr Tyr Thr Pro Pro Tyr Leu Val Asp Cys Ala
1          5          10          15
Tyr Lys Leu Leu Lys Lys His Val Gly Ile Glu Asn Tyr Thr Leu Leu
          20          25          30
Asp Thr Ala Cys Gly Asn Lys Glu Phe Leu Lys Leu His His Pro Lys
          35          40          45
Lys Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn
          50          55          60
Ala Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu
          65          70          75          80
Pro Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe
          85          90          95
Ile Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn
          100          105          110
Asp Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala
          115          120          125
Ile Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu
          130          135          140
Ile Lys Glu Ala Asn Phe Lys Gln Phe Lys Ala Ile
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

697

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837

```

Met Lys Ser Ile Leu Leu Phe Ile Ile Phe Val Val Cys Gln Leu Glu
1      5      10      15
Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr
20      25      30
Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn Asp Leu Ser
35      40      45
Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp
50      55      60
Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr
65      70      75      80
Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr
85      90      95
His Pro Asn Ile Asn Pro Tyr Lys Arg Asn Glu Phe Lys Phe Gln Ile
100      105      110
Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr
115      120      125
Leu Tyr Leu Asp Tyr Thr Gln Thr Asn Trp Phe Gln Ile Tyr Asn Asp
130      135      140
Pro Gln Ser Ala Pro Met Arg Met Ile Lys Phe His Ala
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838

```

Met Gly Leu Met Gly Val Ser Gln Gly Leu Pro Asn Thr Thr Ser Lys
1      5      10      15
Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe Gly Val
20      25      30
Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg
35      40      45
Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg
50      55      60
Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe
65      70      75      80
Ile Gly Ile Pro Ile Pro Ala Ala Val Leu Val Val Leu Cys Val
85      90      95
Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu
100      105      110
Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile
115      120      125

```

SUBSTITUTE SHEET (RULE 26)

698

```

Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile
 130                      135                      140
Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu Glu Ala
145                      150                      155                      160
Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp
                      165                      170                      175
Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser Ala
                      180                      185                      190

```

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839

```

Met Ile Gly Val Tyr Pro Asn Tyr Ser Lys Lys Gln Leu Lys Arg Pro
 1                      5                      10                      15
Leu Val Ile Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu
                20                      25                      30
Thr Asp Ala Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile
                35                      40                      45
Val Met Unk Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu
                50                      55                      60
His Phe Unk Arg Ser Leu Gly Unk Val Phe Asp His Arg Ser Asn His
65                      70                      75                      80
Val Leu Cys Asp Glu Lys Asp Leu Leu Arg
                85                      90

```

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840

Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn His Tyr Cys Arg Lys

SUBSTITUTE SHEET (RULE 26)

699

```

1           5           10           15
Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys Lys Gln Gly Ala Lys
20           25           30
Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Ala Met Ala Ile Ile
35           40           45
Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val
50           55           60
Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro
65           70           75           80
Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile
85           90           95
Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly
100          105          110
Ile Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr
115          120          125
Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Unk Lys Tyr Gly Lys Pro
130          135          140
Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Lys Lys Gly Arg
145          150          155          160
Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Asp Val
165          170          175
Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile Asn Ser Arg Trp Ser
180          185          190
Pro Leu Ser Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val
195          200          205
Thr Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe Val Met Leu Ala Lys
210          215          220
Glu Val Pro Asn Ala His Lys Arg Met Gly Asp Tyr Gly Leu Ala Val
225          230          235          240
Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn
245          250          255
Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu
260          265          270
Cys Ala Ile Leu Arg
275

```

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841

```

Val Leu Thr Ser Gly Asp Met Ile Thr Cys Pro Tyr Cys Gly Arg Ile
1           5           10           15
Leu Tyr Ala Glu Ser Thr His Glu Ser Asn Ala Gln Pro Pro Lys Glu
20           25           30
Ser Gln Pro Lys Glu Ser Gln Glu Glu Ser Gln Glu Glu Ser Gln Glu
35           40           45
Glu Ser Gln Glu Ala Val Arg Leu Ile Val
50           55

```

SUBSTITUTE SHEET (RULE 26)

700

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

```

Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
 1              5              10              15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
      20              25              30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
 35              40              45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
 50              55              60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
 65              70              75              80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
      85              90              95
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
      100              105              110
Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
      115              120              125
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
      130              135

```

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

```

Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
 1              5              10              15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu

```

SUBSTITUTE SHEET (RULE 26)

701

```

      20      25      30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
   35      40      45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
   50      55      60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
   65      70      75      80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
      85      90      95
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
      100      105      110
Arg Unk Ser Phe Ile Val Gly Ala Phe Unk Unk Asn Unk Pro Asp Unk
      115      120      125
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
      130      135

```

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843

```

Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Glu
1      5      10      15
Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu
      20      25      30
Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His
      35      40      45
Leu Glu Leu Ser His Glu Glu Thr Arg Phe Phe Glu Leu Val Gly
      50      55      60
Lys Arg Leu Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp
      65      70      75      80
Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg
      85      90      95
Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln
      100      105      110
Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val
      115      120      125
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser
      130      135      140
Asp Ile Ser Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg
      145      150      155      160
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp
      165      170      175
His Met Pro Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala
      180      185      190
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala
      195      200      205
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe
      210      215      220

```

SUBSTITUTE SHEET (RULE 26)

702

```

Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr
225                230                235                240
Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp
                245                250                255
Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly
                260                265                270
Val Leu Lys Ser Phe Leu Arg
                275

```

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844

```

Met Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu
1           5           10           15
Thr Phe Gly Tyr Ile Val Phe Lys Unk Trp His Tyr Ser Ala Ile Arg
                20           25           30
Leu Ile Val Ile
                35

```

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845

```

Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp Glu Asn Tyr
1           5           10           15
Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu
                20           25           30
Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser
                35           40           45
Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser

```

SUBSTITUTE SHEET (RULE 26)

703

```

      50              55              60
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr
65              70              75              80
Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu Asn Ala Phe
      85              90              95
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile Ala Gly Val
      100              105              110
Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr Leu Lys Lys
      115              120              125
Pro

```

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846

```

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro
1              5              10              15
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg
      20              25              30
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala
      35              40              45
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser Lys
      50              55              60
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His Lys
65              70              75              80
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu
      85              90              95
Ile Ile Ser Asp Ala Asn Lys Glu Ala Leu His Asp His Ala Lys Ile
      100              105              110
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe
      115              120              125

```

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

704

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847

```

Met Arg Val Leu Glu Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp
1      5      10      15
Thr Pro Thr Asn Lys Pro Pro Gln Thr Phe Lys Ile Gln Ile Phe Lys
20      25      30
Ile Gln Ile Gly Ile Ile Asn Asn Phe Asn His Leu Ile Lys Gly Ser
35      40      45
Ser Met Lys Asn Ala Phe Lys Ala Phe Ala Leu Leu Ile Val Phe Phe
50      55      60
Ser Asn Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Asn
65      70      75      80
Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His
85      90      95
Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr
100     105     110
Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp
115     120     125
Ile Ala Arg Pro Lys Lys Leu Tyr Asp Glu Lys Ile Thr Pro Phe Lys
130     135     140
Glu Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asn Leu
145     150     155     160
Lys Met Asp Ser Leu Glu Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile
165     170     175
Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu
180     185     190
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
195     200     205
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
210     215     220
Ala Gln Ile Gly Phe Gly Ala Leu Ser Leu Ile Asp Lys Lys Asp Lys
225     230     235     240
Asn Leu Ser Tyr Phe Ile Ile Asp Lys Thr Leu Tyr Asn Pro Ile Glu
245     250     255
Gln Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys
260     265     270
Val Phe Lys Asp
275

```

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848

Val Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln

SUBSTITUTE SHEET (RULE 26)

705

```

1      5      10      15
Tyr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val
20      25      30
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr
35      40      45
Leu Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser
50      55      60
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met
65      70      75      80
Gly Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe
85      90      95
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile
100      105      110
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
115      120      125

```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849

```

Val Gly Leu Met Lys Ile Arg Phe Met Gly Arg Ser Val Phe Val Gly
1      5      10      15
Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu Phe Trp Leu
20      25      30
Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu
35      40      45
Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys
50      55      60
His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met His Asp Lys
65      70      75      80
Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile
85      90      95
Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe Glu Ala Glu
100      105      110
Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala
115      120      125
Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu Lys Glu Phe
130      135      140
Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Lys Arg Ile
145      150      155      160
Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile
165      170      175
Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly Val Phe Cys
180      185      190
Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys Lys Leu Gln
195      200      205
Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Arg Ser Ile
210      215      220

```

SUBSTITUTE SHEET (RULE 26)

706

Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys
 225 230 235 240
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850

Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser Ala
 1 5 10 15
 Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly Val
 20 25 30
 Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln Phe
 35 40 45
 Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu Pro
 50 55 60
 Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile
 65 70 75 80
 Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys
 85 90 95
 His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys Pro
 100 105 110
 Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser Asn
 115 120 125
 Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val Tyr
 130 135 140
 Ala Leu Glu Val Asn Ala Ala
 145 150

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...154

SUBSTITUTE SHEET (RULE 26)

707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851

```

Val Ile Val Ala Trp Leu Phe Arg Phe Lys Ser Ile Ala Phe Ser Ile
1       5       10      15
Leu Ile Thr Leu Leu Val Ile Leu Val Asp Ile Trp Val Tyr Ser Asp
      20      25      30
Val Arg Gln Phe Leu Leu Asp Thr Ser Ser Ser Phe Ile Trp Leu Leu
      35      40      45
Ile Ala Leu Leu Ile Lys Trp Gly Val Ile Val Ile Ser Ala Arg Lys
      50      55      60
Cys Tyr Gln Phe Ser Gln Lys Met Phe Ala Leu Ile Gln Arg Lys Arg
65      70      75      80
Gln Ile Arg Glu Asn Leu Lys Asn Arg Ser Asn Arg Lys Asp Ala Lys
      85      90      95
Asn Phe Glu Lys Leu Ser Asn Ile Ala Glu Glu Ile Ile Ser Lys Lys
      100     105     110
Gln Glu Glu Ser His His Lys Glu Asp Ser Asn Asp Glu Asn His Lys
      115     120     125
Asp Lys Leu Ser Asn Ile Thr Glu Glu Met Ile Leu Lys Lys Gln Glu
      130     135     140
Glu Leu Lys Ala Arg Lys Asp Lys Gly Asp
145      150

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

```

Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
1       5       10      15
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
      20      25      30
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
      35      40      45
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
      50      55      60
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
65      70      75      80
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
      85      90      95
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
      100     105     110
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
      115     120     125
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
      130     135     140
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
145      150      155     160

```

SUBSTITUTE SHEET (RULE 26)

708

```

Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
      165                      170                      175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
      180                      185                      190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Lys Ser Arg
      195                      200                      205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
      210                      215                      220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
      225                      230                      235
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
      245                      250                      255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
      260                      265                      270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
      275                      280                      285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
      290                      295                      300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
      305                      310                      315                      320
Ser Leu Leu Pro Trp Arg
      325

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

```

Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
1      5      10      15
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
      20      25      30
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
      35      40      45
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
      50      55      60
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
      65      70      75      80
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
      85      90      95
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
      100     105     110
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
      115     120     125
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
      130     135     140
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
      145     150     155     160
Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His

```

SUBSTITUTE SHEET (RULE 26)

709

```

      165      170      175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
      180      185      190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
      195      200      205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
      210      215      220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
      225      230      235
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
      245      250      255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
      260      265      270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Phe Arg
      275      280      285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
      290      295      300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
      305      310      315
Ser Leu Leu Pro Trp Arg
      325

```

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853

```

Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu Unk Ile Ser Glu Gln
1      5      10      15
Pro Glu Val Lys Glu Ile Thr Asn Glu Leu Leu Lys Gln Leu Gln Asn
      20      25      30
Ala Leu Arg Ser Asn Ala His Phe Ser Glu Gln Val Glu Leu Ser Leu
      35      40      45
Lys Cys Ile Val Arg Ile Leu Glu Val Leu Leu Ser Leu Asp Phe Phe
      50      55      60
Lys Asn Ala Asn Glu Ile Asp Ser Ser Leu Arg Asn Ser Ile Glu Trp
      65      70      75      80
Leu Thr Asn Ala Gly Glu Ser Leu Lys Leu Lys Met Lys Glu Tyr Glu
      85      90      95
Arg Phe Phe Ser Glu Phe Asn Thr Ser Met His Ala Asn Glu Gln Glu
      100      105      110
Val Thr Asn Thr Leu Asn Ala Asn Ala Glu Asn Ile Lys Ser Unk Ile
      115      120      125
Lys Unk Leu Glu Asn Gln Leu Ile Glu Thr Thr Thr Arg Leu Leu Thr
      130      135      140
Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp Asn Ala Asn Asn Gln
      145      150      155      160
Ile Thr Lys Asn Lys Thr Unk Ser Leu Glu Ala Ile Thr Gln Ala Lys
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

710

Asn Asn Ser

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

```

Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1           5           10           15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr
           20           25           30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His
           35           40           45
Val Val Phe Gly Thr Gly Arg Gln Glu Asn Leu Gln Lys Leu Gln
           50           55           60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn
65           70           75           80
Lys Pro Glu Thr Lys Arg Ala Ile Glu Thr Ile Phe Ser Met Thr Asp
           85           90           95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
           100          105          110
Lys Ala Tyr Glu Cys Glu Leu Asp Asp Trp Glu Val Met Ile Asp Thr
           115          120          125
Asn Ile Lys Gly Leu Leu His Leu Thr Arg Leu Ile Leu Pro Ser Met
130          135          140
Ile Glu His Asp Gln Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145          150          155          160
Thr Tyr Ala Tyr Pro Gly Gly Unk Val Tyr Gly Ala Ser Lys Ala Unk
           165          170          175
Val Lys Gln Unk Ser Unk Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
           180          185          190
Thr Arg Gly Arg Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
           195          200          205
Ser Arg Val Arg Gly Lys Gly Asp Lys Pro Lys Pro Lys Ser Gly Tyr
210          215          220
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly
225          230          235          240

```

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

711

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

```

Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1           5           10           15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr
          20           25           30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His
          35           40           45
Val Val Phe Gly Thr Gly Arg Arg Gln Glu Asn Leu Gln Lys Leu Gln
          50           55           60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn
65          70          75          80
Lys Pro Glu Thr Lys Arg Ala Ile Glu Thr Ile Phe Ser Met Thr Asp
          85          90          95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
          100         105         110
Lys Ala Tyr Glu Cys Glu Leu Asp Asp Trp Glu Val Met Ile Asp Thr
          115         120         125
Asn Ile Lys Gly Leu Leu His Leu Thr Arg Leu Ile Leu Pro Ser Met
130         135         140
Ile Glu His Asp Gln Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145         150         155         160
Thr Tyr Ala Tyr Pro Gly Gly Unk Val Tyr Gly Ala Ser Lys Ala Unk
          165         170         175
Val Lys Gln Unk Ser Unk Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
          180         185         190
Thr Arg Gly Arg Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
          195         200         205
Ser Arg Val Arg Gly Lys Gly Asp Lys Pro Lys Pro Lys Ser Gly Tyr
210         215         220
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly
225         230         235         240

```

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855

```

Val Phe Ala Thr Asp Ser Ser Ser Phe Ser Met Gly Leu Thr Met Ala
1           5           10           15

```

SUBSTITUTE SHEET (RULE 26)

712

```

Ser Ala Tyr Glu Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln
      20      25      30
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His
      35      40      45
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu
      50      55      60
Gly Arg Phe Val Phe Glu Pro Glu Leu Ala Lys Asn Ile Val Lys Ala
      65      70      75      80
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu
      85      90      95
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr
      100      105      110
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala
      115      120      125
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg
      130      135      140
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe
      145      150      155      160

```

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856

```

Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His
1      5      10      15
Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu
      20      25      30
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp
      35      40      45
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu
      50      55      60
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys
      65      70      75      80
Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro
      85      90

```

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

713

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857

```

Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys Phe
 1             5             10             15
Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu Ser
      20             25             30
Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Lys Asp Ser Ala
      35             40             45
Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly Ile
      50             55             60
Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu Lys
      65             70             75             80
His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala Lys
      85             90             95
Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu Ser
      100            105            110
Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu Lys
      115            120            125
Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln Glu
      130            135            140
Ile Ala
145

```

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

```

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
 1             5             10             15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
      20             25             30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
      35             40             45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
      50             55             60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
      65             70             75             80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
      85             90             95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
      100            105            110

```

SUBSTITUTE SHEET (RULE 26)

714

```

Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu
    115          120          125
Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
    130          135          140
Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys
145          150          155          160
Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Gly Ile Asn Arg Ile
    165          170          175
Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
    180          185          190
Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
    195          200

```

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

```

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1          5          10          15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
    20          25          30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
    35          40          45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
    50          55          60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
    65          70          75          80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
    85          90          95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
    100          105          110
Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu
    115          120          125
Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
    130          135          140
Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys
145          150          155          160
Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Gly Ile Asn Arg Ile
    165          170          175
Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
    180          185          190
Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk
    195          200

```

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

715

(A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859

```

Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
 1           5           10          15
Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
          20          25          30
Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
          35          40          45
Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
          50          55          60
Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
65          70          75          80
Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
          85          90          95
Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
          100         105         110
Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
          115         120         125
Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
          130         135         140
Leu Arg Arg Tyr Ala Tyr Arg Asn Arg Pro Lys Arg Gln Gln Lys Arg
145         150         155         160
Gly Phe Lys Gly Cys Glu Cys Asp Ala Arg Gly Phe Gly
          165          170

```

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860

```

Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly Phe Asp Cys
 1           5           10          15
Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Phe Ile Glu Pro Ser
          20          25          30

```

SUBSTITUTE SHEET (RULE 26)

716

```

Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Ile Pro Lys
   35         40         45
Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu Ile Leu Lys
   50         55         60
Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His Asn Lys Val
   65         70         75         80
Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile Val Gly Ala
   85         90         95
Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp Arg Glu Asn
   100        105        110
Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp Asn Ile Thr
   115        120        125
Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu Lys Lys Lys
   130        135        140
Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys Ala Val Met
   145        150        155        160
Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg His Leu Cys
   165        170        175
Pro Ser Val Thr Ala Cys Lys Lys Ala Cys Leu Thr Phe Arg Met Arg
   180        185        190
Val

```

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861

```

Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val
1         5         10         15
Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro Val Ser Ile Tyr Val
   20         25         30
Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Glu Leu Glu Lys Cys
   35         40         45
Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly Ile Ile Glu Ser Leu
   50         55         60
Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe
   65         70         75         80
Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys Thr Asn Lys Val Glu
   85         90         95
Glu Ile Lys Ala Phe Phe Lys Arg
   100

```

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

717

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862

```

Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys Tyr Phe Leu
1      5      10      15
Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile Asp Ser Leu
20      25      30
Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe
35      40      45
Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser
50      55      60
Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile Lys Ser Asn
65      70      75      80
Gln Tyr Thr Ala Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu
85      90      95
Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val Tyr Val Gly
100      105      110
Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu
115      120      125
Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Glu His Leu Leu Val Lys
130      135      140
Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln
145      150      155      160
Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu
165      170      175
Ser Tyr Ala Glu Ala Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile
180      185      190
Leu His Asp Thr Thr Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly
195      200      205
Ala Asn Ala Leu Asn Thr Thr His Leu Glu Thr Phe Lys Thr Leu Lys
210      215      220
Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala
225      230      235      240
Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln
245      250      255
Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile
260      265      270
Leu Pro Phe Phe Val Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser
275      280      285
Pro Ser Leu Ala Arg Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe
290      295      300
Ile Ile Ile Thr Leu Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys
305      310      315      320
Phe Ser Ile Ser Gly Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro
325      330      335
Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn
340      345      350
Lys Arg Leu
355

```

(2) INFORMATION FOR SEQ ID NO:863:

SUBSTITUTE SHEET (RULE 26)

718

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863

```

Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1           5           10           15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
          20           25           30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
          35           40           45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
          50           55           60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65           70           75           80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
          85           90

```

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863

```

Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1           5           10           15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
          20           25           30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
          35           40           45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
          50           55           60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65           70           75           80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
          85           90

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

```

Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1          5          10          15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
20          25          30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
35          40          45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
50          55          60
Leu Unk Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Unk Leu
65          70          75          80
Ser Unk

```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

```

Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1          5          10          15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
20          25          30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
35          40          45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
50          55          60
Leu Unk Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Unk Leu
65          70          75          80

```

SUBSTITUTE SHEET (RULE 26)

720

Ser Unk

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865

```

Leu Ser Leu Met Unk Val Leu Asn Ala Lys Glu Cys Val Unk Pro Ile
1          5          10          15
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
          20          25          30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
          35          40          45
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
50          55          60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65          70          75          80
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
          85          90          95
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
          100          105          110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
          115          120          125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
          130          135          140
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145          150          155          160
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
          165          170          175
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
          180          185          190
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
          195          200          205
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
210          215          220
Pro Ile Lys Ala Trp Gln Asn Lys Lys
225          230

```

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

721

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865

```

Leu Ser Leu Met Unk Val Leu Asn Ala Lys Glu Cys Val Unk Pro Ile
1      5      10      15
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
20     25     30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
35     40     45
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
50     55     60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65     70     75     80
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
85     90     95
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
100    105    110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
115    120    125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
130    135    140
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145    150    155    160
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
165    170    175
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
180    185    190
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
195    200    205
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
210    215    220
Pro Ile Lys Ala Trp Gln Asn Lys Lys
225    230

```

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866

```

Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala
1      5      10      15

```

SUBSTITUTE SHEET (RULE 26)

722

```

Gln Asn Tyr Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp
      20      25      30
Leu Phe Lys Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys
      35      40      45
Lys Gly Ala Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu
      50      55      60
Lys Met Asp Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu
      65      70      75      80
Glu Ile Met Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn
      85      90      95
Ile Gln Ser Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu
      100      105      110
Asp Glu Leu Leu Gly Leu Lys Asn Thr Leu Lys Asn Leu Pro Leu Tyr
      115      120      125
Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val
      130      135      140
Val Gly Asn Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu
      145      150      155      160
Asn Glu Glu Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro
      165      170      175
Leu Lys Ala His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg
      180      185      190
Ile Asp Tyr Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr
      195      200      205
Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala
      210      215      220
Lys Glu Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867

```

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1      5      10      15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
      20      25      30
Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
      35      40      45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
      50      55      60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
      65      70      75      80
Cys Ile Ser Ser Leu
      85

```

(2) INFORMATION FOR SEQ ID NO:867:

SUBSTITUTE SHEET (RULE 26)

723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867

```

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1           5           10           15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
           20           25           30
Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
           35           40           45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
           50           55           60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
65           70           75           80
Cys Ile Ser Ser Leu
           85

```

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868

```

Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly
1           5           10           15
Ile Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Arg Leu Ser
           20           25           30
His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Val Ala
           35           40           45
Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro
           50           55           60
Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe
65           70           75           80
Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe
           85           90           95

```

SUBSTITUTE SHEET (RULE 26)

724

```

Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala Cys Ile Phe
      100      105      110
Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly Val Leu Leu
      115      120      125
Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser Asp Leu Lys
      130      135      140
Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro Gln Asp Leu
      145      150      155      160
Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn Ile Leu Lys
      165      170      175
Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro
      180      185      190
Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Thr Gln
      195      200      205
Leu Glu Asp Leu Ser Asp Lys Ile Ala Ile Leu Ile Gly Thr Leu Arg
      210      215      220
Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Lys
      225      230      235      240
Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Ile
      245      250      255
Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe
      260      265      270
Ala Arg Ala Leu Ile Tyr Thr Ala Thr Leu Pro Ile Ser Ala Ile Leu
      275      280      285
His

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869

```

Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu
1      5      10      15
Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met
      20      25      30
Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg
      35      40      45
Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro
      50      55      60
Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu Gly Val
      65      70      75      80
Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala
      85      90      95
Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg Glu Val
      100      105      110
Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Glu Arg
      115      120      125
Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn Arg Leu

```

SUBSTITUTE SHEET (RULE 26)

725

130	135	140
Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser Thr Lys		
145	150	155
Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln Ile Leu		160
	165	170
Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys Ala Leu		175
	180	185
Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile Ala Lys		190
	195	200
Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys Leu Glu		205
	210	215
Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser Phe Leu		220
225	230	235
Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser Ala Phe		240
	245	250
Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys Ala Lys		255
	260	265
Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys		270
	275	280
Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile		285
	290	295
Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys Glu Lys		300
305	310	315
Glu Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu Asp Phe		320
	325	330
Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln Arg Ile		335
	340	345
Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly Glu Asn		350
	355	360
Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu Pro Glu		365
	370	375
Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys Pro Ala		380
385	390	395
Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val Arg Asp		400
	405	410
Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile Ala Gly		415
	420	425
Ser Leu Ile Ser		430
435		

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870

Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys
1 5 10 15
His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu
20 25 30

SUBSTITUTE SHEET (RULE 26)

726

```

Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser
   35           40           45
Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala
   50           55           60
Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Thr Tyr Leu Leu Leu
   65           70           75           80
Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala
           85           90           95
Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp
   100           105           110
Phe Leu

```

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871

```

Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
 1           5           10           15
Ile Val Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala
   20           25           30
Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile
   35           40           45
Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu Thr Phe Thr
   50           55           60
Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys Leu Leu Lys
   65           70           75           80
Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly
   85           90           95
Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp
   100           105           110
Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys Lys Gln Leu
   115           120           125
Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met
   130           135           140
Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala Tyr Glu Leu
   145           150           155           160
Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Glu Phe
           165           170

```

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

727

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...115
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872

```

Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1           5           10           15
Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
20           25           30
Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
35           40           45
Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
50           55           60
Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65           70           75           80
Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
85           90           95
Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
100          105          110
Arg Glu Phe
115

```

(2) INFORMATION FOR SEQ ID NO:872:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872

```

Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Unk Ala Met Lys Arg
1           5           10           15
Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
20           25           30
Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
35           40           45
Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
50           55           60
Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65           70           75           80
Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
85           90           95
Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
100          105          110

```

SUBSTITUTE SHEET (RULE 26)

728

Arg Glu Phe
115

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873

Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile	Gly
1				5				10						15	
Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln	Asn
			20					25						30	
Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile	Ser
		35					40					45			
Leu	Val	Unk	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly	Ala
	50				55					60					
Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val	Val
65					70					75				80	
Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Val	Pro	Cys	Phe	Asn	Ser	Phe	Leu
			85						90					95	
Ala	Arg	Ala	Arg	Phe	Cys	Trp	His	His	Phe	Tyr	Gly	Gly	Phe	Ile	Arg
		100					105						110		
Ala	Lys	Arg	Asp	Val	Ser	Tyr	Arg	Lys	Val	Ser	Ile	Leu	Ser	Phe	
	115						120					125			

(2) INFORMATION FOR SEQ ID NO:874:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874

Met	Lys	Pro	Leu	His	Phe	Ser	His	Leu	Asp	Arg	Glu	Gln	Ser	Gly	Asp
1				5					10					15	
Val	Gly	Phe	Ile	Ile	Lys	Asn	Leu	Ile	Phe	Leu	Gly	Val	Phe	Ser	Leu

SUBSTITUTE SHEET (RULE 26)

729

```

      20      25      30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
      35      40      45
Leu Lys Lys Ile Leu Leu Glu Glu Asn Arg Lys Lys Ser Val Leu Glu
      50      55      60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
      65      70      75      80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
      85      90      95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
      100      105      110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
      115      120      125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
      130      135      140
Leu Ile Asn Lys Tyr Leu
      145      150

```

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875

```

Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1      5      10      15
Thr Asp Asp Leu Unk Pro Unk Ser Asp Ala Phe Thr Arg Ser Asp Ile
      20      25      30
Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
      35      40      45
Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
      50      55      60
Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
      65      70      75      80
Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
      85      90      95
Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
      100      105      110
Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
      115      120      125
Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
      130      135      140
Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
      145      150      155      160
Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
      165      170      175
Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Arg Arg Ile Gly
      180      185      190
Ser Val Gln Lys Thr Phe Arg Pro Ser Ser Ala Leu Arg Leu His Phe
      195      200      205

```

SUBSTITUTE SHEET (RULE 26)

730

Ala

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876

```

Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp Leu Ile Lys
1      5      10      15
Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala Ser Gly Val
20     25     30
Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly Met Glu Leu
35     40     45
Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Unk Val Gly Leu
50     55     60
Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val Cys Asp Lys
65     70     75     80
Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly Asn Leu Ala
85     90     95
Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile Glu Asn Tyr
100    105    110
Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys Ile Asn Arg
115    120    125
Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp Val Gly Thr
130    135    140
Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met Met Glu Phe
145    150    155    160
Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro Asn Asn Pro
165    170    175
Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu Ala Ser Gly
180    185    190
Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser Ile Leu Asn
195    200    205
Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn His Thr Leu
210    215    220
His Leu Ile Ala Ile Ala Asp Leu Val Gly
225    230

```

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

731

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

```

Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
1      5      10      15
Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu
20     25     30
Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile
35     40     45
Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn
50     55     60
Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg
65     70     75     80
Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu
85     90     95
Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
100    105    110
Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
115    120    125
Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met
130    135    140
Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro
145    150    155    160
Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
165    170    175
Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
180    185    190
Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
195    200    205
Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
210    215    220
Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
225    230    235    240
Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu
245    250    255
Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
260    265    270
Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe
275    280    285
Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
290    295    300
Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn
305    310    315    320
Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys
325    330    335
Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
340    345    350
Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
355    360    365
Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu
370    375    380
Arg Phe Asn Asn Glu Gly Cys Gly Asn
385    390

```

(2) INFORMATION FOR SEQ ID NO:877:

SUBSTITUTE SHEET (RULE 26)

732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

```

Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
1      5      10      15
Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu
20      25      30
Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile
35      40      45
Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn
50      55      60
Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg
65      70      75      80
Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu
85      90      95
Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
100      105      110
Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
115      120      125
Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met
130      135      140
Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro
145      150      155      160
Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
165      170      175
Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
180      185      190
Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
195      200      205
Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
210      215      220
Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
225      230      235      240
Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu
245      250      255
Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
260      265      270
Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe
275      280      285
Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
290      295      300
Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn
305      310      315      320
Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys
325      330      335
Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
340      345      350
Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
355      360      365
Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu

```

SUBSTITUTE SHEET (RULE 26)

733

370 375 380
 Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn
 385 390

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

```

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1          5          10          15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
20          25          30
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
35          40          45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
50          55          60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65          70          75          80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
85          90          95
Unk Phe Lys Arg Cys Lys
100

```

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

```

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1          5          10          15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
20          25          30

```

SUBSTITUTE SHEET (RULE 26)

734

Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
 35 40 45
 Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
 50 55 60
 Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
 65 70 75 80
 Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
 85 90 95
 Unk Phe Lys Arg Cys Lys
 100

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879

Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys
 1 5 10 15
 Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn
 20 25 30
 Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile
 35 40 45
 Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu
 50 55 60
 Lys Tyr Ser Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser
 65 70 75 80
 Val Ala Glu Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys
 85 90 95
 Gly Leu Ile Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala
 100 105 110
 Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu
 115 120 125
 Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val
 130 135 140
 Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly
 145 150 155 160
 Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys
 165 170 175
 Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr
 180 185 190
 Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu
 195 200 205
 Asn Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile
 210 215 220
 Ser Asn Val Val Leu Val Ile Ala Lys Ala Arg Ala Glu Ile Ser Cys
 225 230 235 240
 Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Glu Leu
 245 250 255
 Ala Asn Glu Arg Glu Arg Glu Arg Glu

SUBSTITUTE SHEET (RULE 26)

735

260

265

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

```

Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
1      5      10      15
Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
20     25     30
Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
35     40     45
Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
50     55     60
Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
65     70     75     80
Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
85     90     95
Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
100    105    110
Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
115    120    125
Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
130    135    140
Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
145    150    155    160
Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
165    170    175
Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
180    185    190
Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
195    200    205
Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
210    215    220
Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
225    230    235    240
Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
245    250    255
Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
260    265    270
Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu
275    280    285
Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
290    295    300
Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser
305    310    315    320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
325    330    335

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SUBSTITUTE SHEET (RULE 26)

736

Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
 340 345 350
 Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk
 355 360

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Unk Phe Leu Asn Thr Gln
 1 5 10 15
 Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
 20 25 30
 Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
 35 40 45
 Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
 50 55 60
 Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
 65 70 75 80
 Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
 85 90 95
 Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
 100 105 110
 Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
 115 120 125
 Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
 130 135 140
 Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
 145 150 155 160
 Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
 165 170 175
 Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
 180 185 190
 Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
 195 200 205
 Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
 210 215 220
 Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
 225 230 235 240
 Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
 245 250 255
 Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
 260 265 270
 Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Asn Leu
 275 280 285
 Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
 290 295 300
 Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser

SUBSTITUTE SHEET (RULE 26)

737

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305          310          315          320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
          325          330          335
Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
          340          345          350
Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk
          355          360

```

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995

```

GACGCACGTA GTTCTTTTIT AAGATTGGTA GCTATGGCAT TATGTTTGAT CTTAATTAAT      60
AGTAGAGGAG TAGCGATGGG ATACGCAAGC AAATTAGCTT TAAAGATTG TTTGGTAGGT      120
TTATGTTTAT TTAGCACCTT TGGTGACGAA CACCTTGAGC AAAAAGGGAA TTATATTTAT      180
AAGGGAGAGG AGGCTTATAA TAATAAGGAA TATGAGCGAG CGGCTTCTTT TTATAAGAGC      240
GCTATTAAAA ATGGTGAGTC GCTTGCTTAT ATTCTTTTAG GGATCATGTA TGAAAATGGT      300
AGGGGTGTAC CTAAAGATTA CAAGAAAGCG GTTGAATATT TCCAAAAAGC TGTGATAAC      360
GATATACCTA GAGGGTATAA CAATTGGGC GTGATGTATA AAGAGGGTAA GGGAGTTCCT      420
AAAGATGAAA AGAAAGCGGT GGAATATTTT AGAATAGCTA CAGAGAAAGG TTATACTAAC      480
GCTTATATCA ACTTAGGCAT CATGTATATG GAGGCGAGG GAGTTCCAAG TAACTATGCG      540
AAAGCGACAG AATGTTTTAG AAAAGCGATG CATAAGGGCA ATGTGGAAGC TTATATTCTC      600
CTAGGGGATA TTATTATAG CGGGAATGAT CAATTGGGTA TTGAGCCGGA CAAAGATAAG      660
GCTGTTGTCT ATTATAAAAT GCGCGCCGAT GTGAGTTCTT CTAGAGCTTA TGAAGGGTTG      720
TCAGAGCCTT ACCGGTATGG GTTAGGCGTG GAAAAAGATA AAAAAAGGC TGAAGAATAC      780
ATGCAAAAAG CATGCGATTT TGACATTGAT AAAAATTGTA AG                                822

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(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

738

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996

ACGATGAAAA ATACATCGTC ATCAACGACT TTAACAATGA ATGACACCAT TGCCGCTATC	60
GCTACCCCTT TAGGCAAGGG AGCGATTAGC ATCATTAAAA TCAGCGGCCA TAACGCCCTA	120
AACATCCTCA AACAACTCAC CCAAAAACAA GACTTCACCC CCAGATACGC TTACGTGTGC	180
GACATTTTTT CTGATGGCGT TTTATTGGAC AAAGCGTTAG TGATTATTAT CAAAGCCCCC	240
TATAGTTTCA CCGGTGAAGA TGTGTGCGAA ATCCAATGCC ATGGAAGCCC CCTTTTAGCG	300
CAAAATATCC TTCAAGCTTG CTTGAATTTA GGGGCTAGGC TCGCTAAAGC GGGGGAATTT	360
AGCAAAAAG CCTTTTAA CCATAAAATG GATTTGAGCG AGATTGAAGC GAGCGTTCAG	420
CTCATCCTTT GTGAAGATGA AAGCGTT	447

(2) INFORMATION FOR SEQ ID NO:997:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997

AATCTAATTT ATCGGAGCTC ACAAAGGAGC GCAGCCGCTT GCGTGGTGCG TTTGAATAAA	60
GAGCCGATGA TTGAATACTT GAAATCCAAT ATCAAGCTCA TTGATGAGAT GATTGCAAGC	120
GGTTATGAAG ACAAAGAGAC TTTGAAAAAA CGCAGAGATG CGATGCAAGC TTGGGTGGAT	180
AAGCCGGTAT TGTTAGAGCC AGATAGTAAC GCCCAATACG CCGCTGTTCAT TGAATTTGAT	240
GTGGCAGAAA TCACGGAGCC TATTTTGGCA TGCCCTAATG ACCCTGATGA CGTCGCTACT	300
TTGAGCGAAG TTTTAGCGGA TACGACCGGC AAAAGACCCC ACGCTATTGA TGAAGTGTTT	360
ATTGGCTCTT GCATGACGAA TATTGGGCAT TTCAGAGCCT TTGGTGAAAT CGTTAAAAAC	420
GCCCCTCCCA GTCAAGCAGC CCTTTGGGTA GTGCCACCCA GTAAAAATGA CGAACAAGAG	480
CTTATTAATG AGGGCTATTA TCGGATTTT GGGGCTGCCG GGGCAAGGAC TGAAGTACCA	540
GGCTGTAGCT TGTGCATGGG CAATCAAGCG AGGGTTAGGG ATAATGCGGT CGTTTTTTCT	600
ACTTCCACAC GGAATTTTGA TAATCGTATG GGTAGAGGGG CTAAAGTGT TTTGGGCAGT	660
GCGGAGCTTG GGGCGGCGTG CGCTTTACTA GGGAGGATCC CCACTAAAGA AGAATACATG	720
AATTTAGTGA GTGAAAAGCT AGAGAGCCAA AAAGACAAGA TCTATCGCTA CATGAACTTT	780
AACCTAATGG AGAATTCAG GCTC	804

(2) INFORMATION FOR SEQ ID NO:998:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

739

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998

AAAATGCCAT	ACGCCTTAAG	AAAAAGATTT	TTCAAACGCC	TTTTATTGTT	TTTTTTAATT	60
GTTTGTATGA	TAAATTTGCA	TGCCAAAAGC	TATCTGTTTT	CTCCTTTGCC	CCCAGCGCAC	120
CAGCAAATCA	TTAAGACAGA	GCCTTGCTCT	TTGGAGTGCT	TGAAAGACTT	GATGCTGCAA	180
AATCAAATCT	TTCTTTTTGT	ATCCCAATAC	GATGATAACA	ACCAAGATGA	GAGCCTTAAA	240
ACTTATTACA	AGGACATCTT	AAACAAACTC	AACCCCGTAT	TCATCGCTTC	TCAAACTCCA	300
GCTAAAGAAA	GCTATGAGCC	TAAGATTGAA	CTTTAGCGTT	TACTGCCTAA	AAAGGTGGTG	360
GGCCGTTATG	CGATTTTAGT	GATGAACACC	TTTTAGCGT	ATTTGAACAC	CAGAAACAAC	420
GATTTCAATA	TCCAAGTCTT	TGACAGCGAT	GAAGAAAGCC	CTGAAAAATT	AGAAGAAACC	480
TATAAGAAA	TTGAAAAAGA	AAAATTCCTT	TTTATCATCG	CTTTATTGAC	TAAAGAGGGC	540
GTGGAAAATT	TGCTCCAAA	TACGACTATC	AATACCCCTA	CTTATGTGCC	TACGGTGAAT	600
AAAACGCAAT	TAGAAAATCA	TACCGAGCTT	TCTTTAAGCG	AGCGCTTGTA	TTTGGGGGGG	660
ATTGATTATA	AAGAGCAATT	AGGCATGCTC	GCAACTTTCA	TTAGCCCTAA	TCGCCCCGTG	720
ATTGAATACG	ATGATGATGG	CCTGATAGGT	GAACGCTTGA	GGCAAATCAC	GGAGTCTTTA	780
AACGTTGAAG	TCAAACACCA	AGAAAACATT	TCTTACAAAC	AAGCGACCAG	TTTTTCTAAA	840
AATTTTAGAA	AACATGATGC	GTTTTTTAAA	AATTCTACCT	TAATTTTGAA	CACCCCTACC	900
ACTAAAGCG	GTCTGATCCT	TTCTCAAATA	GGGCTTTTAG	AGTATAAGCC	TCTTAAAATC	960
CTTTCCACAC	AAATCAATTT	CAACCCCTCT	TTACTCTTGC	TCACCCAGCC	TAAAGACAGG	1020
AAAAATTTAT	TCATTGTCAA	TGCCTTGCAA	AACAGCGATG	AAACGCTGAT	AGAATACGCT	1080
TCCTTATTAG	AGAGCGATTT	AAGGCATGAT	TGGGTGAATT	ATTCCAGCGC	GATAGGGCTA	1140
GAGATGTTTT	TAAACACGCT	AGATCCGCAT	TTTAAAAAGT	CTTTTCAAGA	GAGTTTGGAA	1200
GACATCAAG	TCCGTTACCA	CAATCAAATT	TATCAGGCTT	TAGGGTATTG	TTTTGAGCCG	1260
ATAAAAAACG	AAAGCGAAAC	AAAAAAGAA				1290

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1458 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999

TATTTAGATA	ATTATTTGAA	TACTTTTATT	TTTAATGGGT	TTTTAAGAAA	GATAGACTAT	60
TATGCGAGTG	GGAAATTAAA	AAGGATTGGT	GCGGTGTTAA	AATTTCAAAA	ATTACCCCTTA	120
TTGTTTGTIT	CCATTCTTTA	TAATCAAAGC	CCTTTATTGG	CTTTTGATTA	TAAGTTTAGT	180
GGGGTAGCGG	AATCTGTTTC	TAAAGTGGGG	TTTAACCATT	CCAACTCAA	TTCCAAAGAA	240
GGGATTTTCC	CTACAGCCAC	CTTTGTAACC	GCCACGATCA	AGCTTCAGT	GGATTCCAAT	300

SUBSTITUTE SHEET (RULE 26)

740

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CTGCTCCCTA AAAACATTGA AAAACACAGC TTAAAAATAG GCGTTGGGGG GATTTTAGGA 360
GCGCTCGCTT ACGATTCCAC CAAAACGCTC ATAGACCAAG CCACGCATCA AATCTATGGC 420
TCAGAACTTT TTTACCTCAT AGGGCGTTGG TGGGGGTTTT TAGGCAACGC TCCTTGAAA 480
GACTCCCTCA TAGAATCTGA CGCTCACACC CGTAATTATG TGCTGTATAA TTCCTATCTG 540
TTTTATTCTT ATGGCGATAA ATTCCACCTA AAATTAGGGC GTTATCTCTC TAACATGGAT 600
TTTATGAGTT CCTACACACA GGGTTTTGAA CTGGATTATA AAATCAATTC TAAAATAGCG 660
TTAAATGGT TTAGCTCTTT TGGGAGGGCG TTGGCTTTTG GGCAATGGAT ACGGGATTGG 720
TATGCCCTTA TTGTAACCTGA AGATGGCAGA AAAGAAGTTT ATGATGGCAT CCATGCCGCG 780
CAACTCTATT TTTCTAGCAA GCATGTTCAA GTCATGCCTT TTGCTTATTT TTCGCCTAAG 840
ATTTACGGAG CGCCCCGTGT TAAAATCCAT ATTGATAGCA ACCCGAAATT CAAAGGCTTA 900
GGGTTAAGGG CTCAAACAC TATTAATGTG ATTTTCCCTG TTTATGCTAA AGATTATATAC 960
GATGTGTATT GCGCTAATC TAAGATTGGC GAGTGGGGCG CATCGCTTTT GATCCACCAA 1020
CGCTTTGACT ACAACGAATT TAACTTTGGC TTTGGTTATT ACCAAAATTT TGGCAACGCT 1080
AACGCAAGGA TTGGCTGGTA TGATAACCCC ATCCCTTTTA ATTATAGAAA TAACAGCGTT 1140
TATGGTGGGG TCTTCAGTAA CGCTATTACC GCAGACGCCG TTTCTGGGTA TGTCTTGGT 1200
GGGGGGGTGT ATAGAGGGTT TTTATGGGGT ATTTTAGGCA GATACACTTA TGCCACTAGA 1260
GCGAGCGAAA GATCCATCAA CTTGAACCTG GGCTATAAAT GGGGTTCTTT TGCTAGAGTT 1320
GATGTGAATT TAGAATACTA TGTGGTCAGC ATGCACAACG GCTATAGATT AGACTATCTC 1380
ACCGGCCCTT TCAACAAAGC CTTAAGGCT GACGCACAAG ATAGGAGTAA CCTTATGGTT 1440
AGCATGAAAT TCTTTTTT

```

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000

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GTTTACGCGG GGTGGCTAT CGCTATAGGC ATGCTCATTG ACTCATCTGT GGTAGTGGTG 60
GAAAACGCTT TTGAAAAATT GAGCGCTAAC ACTAAAACCA CTAACTCCA TGCAATCTAT 120
CGTTTCATGCA AAGAAATCGC CGTTTCAGTG GTGAGCGGGG TGGTGATCAT TATTGTGTTT 180
TTTGTGCCGA TTCTAACCTT ACAGGGGTTA GAGGGCAAGA TGTTTAGGCC TTTAGCGCAA 240
AGCATTGTGT ATGCGCTTTT AGGCACTTTA GTTCTATCCA TCACTATCAT TCCTGTAGTG 300
AGCTCTCTTG TCTTAAAGC CACGCCCCAT AGCGAAACCT TTTTAACGAG GTTTTTTAAAC 360
AGAATCTACG CCCCTTTATT GGAATTTTTT GTGCATAACC CTAAAAAAGT GATTTTAGGA 420
CCGTTTGTGT TTTTAATCGC AAGCCTTTCT TTATTCCTT TTGTGGGGAA GAATTTTCATG 480
CCTGCTTTAG ATGAGGGCGA TGTGGTTTGT AGCGTGGAAA CCACCCCTC TATTTCTTA 540
GATCAATCTA AAGATCTCAT GTTAAACATT GAAAGCGCGA TTAAAAAGCA TGTCAAAGAA 600
GTTAAAAGCA TTGTCGCGCG CACAGGGAGC GATGAATTGG GGCTGGATTT AGGGGGTTTG 660
AATCAAACCG ATACTTTTAT TTCTTTTCATC CCTAAAAAG AATGGAGCGT TAAAACCAA 720
GATGAATTGG TTAGAAAAAA TCATGGATTG TTTAAAGAC TT 762

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(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

741

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001

TGGTTGTTTC	TAACATGCTA	TGGTAGTGTG	ATAAAGAAAG	GCTATATAAG	AGGAGATCTT	60
ATGCCGTATAG	TTAGAAATTT	ATTTCCTTGT	TCGTTTGTGG	CGTATAGTAG	TGCCTTCGCA	120
GCGGATTTAG	AAACCGGAAC	CAAAAACGAC	AAAAAGAGCG	GTAATAAAATT	TTACAAACTC	180
CATAAAACC	ATGGCTCAGA	AACCGAGACT	AAAAACGATA	AAAAGCTTTA	TGATTTCACT	240
AAAAATAGCG	GATTAGAAGC	CGTGGATTTA	GAAAAAGCC	CTAACCTTAA	AAGCCATAAA	300
AAAACGGATA	AAAAGTTTTA	TAAACAACTC	GCTAAAAACA	ATATCGCTGA	AGGGGTGAGC	360
ATGCCGATTG	TGAATTTCAA	TAAAGCCCTA	TCTTTTGGGC	CTTATTTTGA	AAGGACTAAA	420
AGCAAAAAAA	CCCAATACAT	GGACGGCGGG	TTGATGATGC	ACATCCGTTT	T	471

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002

CCGAAAAATTG	CACCGCTTGC	CATGGCATT	AATCCCAAAA	CATTCCAGCC	CCTATGGATA	60
GCCTTAGTGC	GAGCAACTCT	TTTGGGGTGG	GGCCACCGGA	ATTTAAGCCA	TGTGGCGGGG	120
GTTTTGAACG	CGAGTTTCTT	AGCCCACTTC	ATCAAAGACC	CGGTGAAAAC	GGCGAAATTG	180
AGCCATAAGT	TCAACGATGA	AAGGCCCTAT	CCTATGCCGG	CGTTTTCTCA	ATTAGCGAT	240
CAAGATTTGA	GCGATATTGT	GGCGTATCTC	ACTTCTATTT	TGCCTAAAAA	TTTGAGCGAT	300
AAGGAAGTGT	TCGCGCAAAG	TTGTCAAAGG	TGCCATAGCC	TGGATTATGC	TAAAGATAAG	360
GCCTTTAGCG	ATCCTAAAGA	TTTAGCCAAT	TATTTAGGCT	CTCATGCGCC	TGATTTGTCC	420
ATGATGATTA	GGGCTAAGGG	CGAACATGGC	TTGAATGTTT	TCATCAACGA	TCCGCAAAAG	480
CTTTTGCCTG	GCACAGCCAT	GCCTAGAGTG	GGATTGAATG	AAAAAGCTCA	AAAACAAGTC	540
ATTTCTTATT	TGGAAAAAGC	GGGCGATAGG	AAAAAGCATG	AAAGGAATAC	TTTAGGGATT	600
AAGATCATGA	TTTTCCTTGC	GGTGTGTCTG	TTCTTGGCTT	ACGACTGGAA	AAGAAAAGTT	660
TGGAGCGAAG	TGCAT					675

SUBSTITUTE SHEET (RULE 26)

742

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003

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ACTTGGCGGT ATCAACTAGG CTCATTAAAA GGCAAAATCC AAATGATTAA AAGCGTAGAG      60
ATTGAAAATT AAAAAAATTT TGAGCACCTT AAAATGGAAA ATTTTAAACT CATCAACTTT      120
TTTACCGGTC AAAACGATGC GGGTAAAACC AATCTTTTAG AAGCTCTTTA TACCAACACA      180
GGCCTTTGTG ATCCTACTGC CAATCAAGTC AGTCTTCCTC CTGAACATGC CGTGAATATT      240
AGTGAATTCA GAAAAATCAA ACTCGATGCC GACAACCTAA AAACCTTTTT TTATCAAGGA      300
AACACCGCTA ATCCCATTAG TATCCGCACT GAATTTGAAC ATGCTACTAT CCCTCTTACT      360
ATCCAATACC CCACACAAAC CAGTTACAGC AAAGACATCA ATTTGAATAG CGATGATGCT      420
CATATGACAA ACCTTATAAA CACAACAATA ACGAAGCCAC AGCTCCAATT TTCCTACAAT      480
CCATCCCTTT CCCCCATGAC AATGACTTAT GAATTTGAAA GGCAAAACCT AGGTTTAATC      540
CATTCTAATT TAGATAAAAT CGCTCAAACC TATAAAGAAA ATGCGATGTT TATTCCTATA      600
GAATTATCTA TTGTTAATTC TCTTAAAGCA TTGGAAAATT TACAATTAGC AAGCAAAGAA      660
AAAGAATTGA TTGAAATCCT ACAATGTTTC AACCCATAA TTTTAAATGC TAATACAATA      720
AGAAAGTCTG TCTATATCCA AATCAAAGAT GAAAACACAC CGCTAGAAGA AAGTCCCAAA      780
AGGCTTTTAA ATTGTTTGG TTGGGGTTTT ATCAAATTCT TTATTATGGT GAGCATTCTT      840
ATAGACAATC GTGTCAAGTA TCTTTTATT GATGAAATAG AAAGCGGTTT GCACCATACA      900
AAAATGCAAG AGTTTTTAAA AGCTCTGTTT AAGTTAGCTC AAAAATTACA GATTCAAATT      960
TTTGCCACCA CGCACAATAA GGAATTTTAA TTAAACGCCA TCAACACGAT ATCCGATAAT     1020
GAAACGGGAG TTTTAAAGA CATAGCCTTG TTTGAGCTTG AAAAAGAAAG CGCTTCTGGC     1080
TTTATCAGAC ACAGCTATTC TATGCTAGAA AAAGCGCTTT ATAGGGGTAT GGAGGTTAGA     1140
GGC                                                                    1143

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(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...852

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004

ACCCATTGTT TATTCCTTGG TGGTAGTATC AAAATTTTGT TAATCCTTAA AGAGGGCATT	60
GATTTAAACC ATGGTTATTA CCAATTAGGA AAATACACCA TTAAAGACGA CTTTATCCCC	120
AGTAAAAAGG CCGTGTGGA AGACGTTTG ATCCAATCTA GCAATGTGGG CATGATAAAA	180
ATCAGTAAAA GCCTCAACCC AGAGGATTTT TATAACGGGC TTTTAGGCTA TGGATTTTCT	240
CAAAAACCG GCATTGATTT ATCCTTAGAA GCCACAGGAA AGATCCCTCC TTTGTCCGCT	300
TTCAAGCGTG AAGTGTAA GGGGAGCGTC TCTTATGGCT ATGGGTTGAA TGC GACTTTT	360
TTGCAGCTTT TAAGGGCTTA TCGGTGTTT TCTAATGAAG GCAAATTGAC TACCCCTAT	420
TTAGTGCAAC GAGAAACCGC CCCTAATGGC GATATTTACA TCCCTAGCCC CAAACCCACC	480
TTCAAGTCA TTAGCCCCAA AAGCGCTAGA AAAATGAAAG AAACCTTAAT TAAGGTGGTG	540
CGTTATGGCA CAGGCAAAAA CGCTCAATTT GAAGGGCTAT ACATAGGGGG CAAAACAGGC	600
ACGGCTAGGG TTGCTAAAAA CGGAAGCTAT AGCGCGGAGT CCTATAACAG CTCCTTTTTT	660
GGGTTGCTG AAGATGAAAG GCAGGTTTTT ACTATCGGCG TGTTATCTT AGGCTCGCAT	720
GGCAAGGAAG AGTATTACGC TAGCAAGATT GCAGCCCCCA TTTTAAAGA AATCACCGAA	780
ATTTTAGTGC GTTACAATTA CCTATCGCCC TCTATTGCGA TTCAAACGC TTTGGA AAAA	840
AACCGCTTAA AA	852

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005

GATAAAAAA TACTTTTAAT TATTCAAGGA AAATTTATGG AATTTTCATCA AGTTTATGAC	60
CCATTAGGCC ATATTGGCT GAGCGCTTTA GTCGCACTTT CGCCTATTGC GCTCTTTTTT	120
ATCTCTCTTA TTGCTTTAA ACTTAAAGGG TATAGCGCTG GGTTTTAAAG CTTAGCGCTT	180
TCAATCCTTA TTGCGTTATT TGTGTATAAA ATGCCTGTTT AAATGGTGAG CGCGAGTTTT	240
TTCTATGGCT TTCTTTATGG CTGTGGCCG ATCCCATGGA TTGTGATCGC TCGGATTTTT	300
CTTTACAACC TTTCACTGAA GTCCGGGTAT TTTGAAATCT TAAAAGAAAG CGTTCAGTCC	360
ATCACTTTAG ATCACCGCAT TTAGTGATT TTGATTGGCT TTTGTTTGGC TCATTTT	417

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

744

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006

CCTAAACCTA AAGGGGTTTG CCCTAAAAAT CTAATGAGTA AAAGAGCGAT CCGTTTCCCT	60
AACAAGCTTT TTTTCATACCC TAAACCCAAA ATAAAAGCGA CAAACACAAG CCACACCGTT	120
TTATTTCGCAT ACCCGCTCAA ACCCCACGAA ATGGCCTTAT TAGCGCTCGC TACCTCACTG	180
CTCGCTCCAA TTTTAAACGC TATACACAGC ACTAACGCGC TCAACGCTAT CAAACCTGAT	240
GGCACCGGCT CTAATAATTAA CCCTATAATC ATGCCCATGA AAATACAAAA A	291

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007

AGAAACGATT TTAAAGGTGT TAGAAAAATG GCATTAAGGG TATTATTATT CTTTTGTTTT	60
TTGTTTTTGC AAGCAGAAGA TAAGAGCCAA GAATTATCAT CTATACAAAA ACAAAATGGCT	120
TTGGTGGATA AAAAAGCTCGC CAAAGACGAT AACGTGTGGT TGAAAAAATT TGAAAACTAT	180
AAAATTTTACA ACCAAATTTA TACTGAAAAA GAGAGCGTGA GGCAGGAATT AAGGCGCTTA	240
AAAAACAAAA AAAGCAAGGA TTTATTAAAG ATTAGCACCT TAGAGCATAC CTTAAAGGCT	300
TTAGAGTCCC AGCAAAAAAT GTTTGAAAGC TATGGGGTCA ATCCTTTTAA GGAATTGATA	360
GAGCGCCCCA ATATCCCCAA TATCCCTAAT ATCGCTAACC CTATTGCGAT CATTGATGGC	420
ATTTCTTTTCA TCAAGAGCAT GCGTTTAAAG CATGAAAATC TTAAAAATAA CCAGACTTCT	480
TTAGGAGAAG TTTTAAAGCT TTTAGATCAA AAACACCAGC TTTTAAATCA GTGGCACGCT	540
TTGGATAAAA GCGCGAAATT AAGCGATGAG ATTTATCAAA CTCAAGCCAA ACGCTTAGAA	600
TTGCAAGGGG CTCAAAAAT TCTAAAAACC ACGATCGGGA TTTTCCAAAA AGACAGCGAT	660
GAAGCTATAA GCATTGTCAA ATCTCAAGTT AAAAACCAGC TTTTAAATT GGTTTATGTG	720
TTTTTAGCGG CCTTTTGAG CGTGGTGTTC GCGTGGATTT TAAAAATCAT TTCCAGTAAA	780
TACATTGAAA ATAATGAGCG CGTCTATACC GTGAATAAAG CCATTAACTT CGTGAATGTG	840
AGCGTGATCG TTTTAATCTT TCTTTTCTT TATTTAGAAA ACGTTACTTA CTTGGTAACG	900
GTTTTAGGCT TTGCGAGCGC GGGCTTAGCG ATTGCGATGA AGGATTATT CATGAGCTTG	960
CTCGGGTGGT TTATCATTTT GATTGGGGGG AGCGTGCATG TGGGCGATAG GGTGCGTATC	1020
GCTAAGGGGA CGGATATTTT TATTGGCGAT GTGTTGGATA TTTCTATGTT GCACATTACG	1080
ATTTTAGAAG ACGTAACCTT TACCACCTAC ACGAATAACA GGAGAGCGGG CCGAATTATC	1140
TTTGTGCCTA ACAATTACAT TTTCACCACC ATGTTTCGCTA ATTACAGCCA TTTTGGGATG	1200
AAAACGGTTT GGGATGGCGT GGATTTTTCG GTTACATTTC ATTCTGATTT TAAAAAAGCG	1260
TCTAAAATTG CGCTCAATAT CGCTACGGAA TTGTCTAAAG AATACACGGA TATTACCTAT	1320
AAACAGCTCA ATAAATGCG CGACCGGTAT TCTTTAAGGA GTTTGAGCGT CAAGCCTCGA	1380
TGCTTTTGA TGCCTGAAAA TAACGGGATA AAAATCTCGG TGTGGTATCA AACCAATTCC	1440
TATGCCACCA TGTCTTTAAG GAGCAAGATT GTGGCTGAAA TTGTTGAAGC CTTTTTGAAA	1500

SUBSTITUTE SHEET (RULE 26)

GAAGAAAATA TCCATATCGC TTATACGACC AGCAAGCTGC TTAAAGTGGA TGCTGATGCT 1560
CTAGGCGATG GTTTTGGGAA TAAAGCGGAA CAAAAA 1596

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008

CGGAGTGAAA	GAATGCAAGA	AATCTTAATC	CCTTTAAAAG	AAAAAAGCTA	TAAAGTGTTT	60
TTGGGGGAAC	TGCCTGAAAT	AAAATTGAAA	CAAAAAGCGC	TCATCATTAG	CGATAGCATC	120
GTGGCCGGGT	TGCATTGCCC	CTATTGTGTA	GAGCGCTTGA	ACGCCCTTAG	AGTCAGAGTG	180
TGCGTGATAG	AGTCCGGGGA	AAAATACAAA	AATTTTCATT	CATTAGAGCG	GATTTTAAAC	240
AACGCCTTTG	AAATGCAATT	AAACCGCCAT	TCTTTAATGA	TAGCCCTTGG	TGGGGGAGTG	300
ATAAGCGATA	TGGTGGGGTT	TGCGAGCAGT	ATTTATTICA	GGGGGATTGA	TTTTATTAAT	360
ATCCCTACGA	CTTACTCGC	TCAAGTGGAT	GCGAGCGTGG	GGGGGAAAAC	AGGGATCAAC	420
ACGCCCTTATG	GCAAGAACCT	AATCGGATCG	TTCCACCAGC	CTAAAGCGGT	TTATATGGAT	480
TTAGCTTTTT	TAAAAACCCT	TGAAAAAAGG	GAATTTCAAG	CGGGGGTTGC	TGAAATCATT	540
AAAATGGCGG	TGTGTTTTGA	TAAAAACTTG	GTAGAAAGAT	TAGAAACAAA	GGATTTAAAA	600
GATTGTTTAG	AAGAAGTAAT	CTTTCAAAGC	GTCAATATCA	AAGCTCAAGT	CGTTGTTCAA	660
GATGAAAAAG	AGCGAAACAT	CAGGGCTGGG	TTGAACTATG	GGCATACCTT	TGGCATGCTG	720
ATAGAAAACG	AGACCAATTA	CGAGCGATTT	TTGCATGGCG	AAGCGATCGC	TATTGGCATG	780
CGCATGGCTA	ATGATTTAGC	CCTTCTTTTA	GGCATGCTCA	CTTTAAAAGA	ATACGAACGC	840
ATAGAAAATT	TATTGAAAAA	ATTTGATCTG	ATATTCAATT	ACCAAATCAC	TGATATTCAA	900
AAATTTTACG	AACGCTTGTT	TTTAGACAAA	AAAAGCGAGA	ACCAAACCCT	AAAATTCATT	960
TTGCCTAAAG	GTGTTGGAGC	GTTTGAGATT	GCCTCTCATA	TCCCTAAAGA	AACGATTTTA	1020
AAGGTGTTAG	AAAAATGCA	T				1041

(2) INFORMATION FOR SEQ ID NO:1009:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

746

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009

AAATCAAAGA	GTATGAAATT	AAGGAGAGGG	AAATCATGCG	CGTTTTCTAA	ATTTTATAGAA	60
AACCTCACCG	CTCCCTTTAA	ACGCATCAAA	AACCGCTCGC	TTGTTTTGGC	GTTAGGGTTT	120
TTGATCCTTA	CTTTTGGCTT	GTTGCTTTTT	TTAATCTTAA	GCGATGTTTC	TAGGCTCATA	180
TCCAGTAAGG	ATTTTCTTTA	TGTGATCCAG	TCTCACCCCTA	AACAAACTCT	AATTGAAGAT	240
GAAAATTATT	TTTATGCTAA	CAAGGGTCTT	TATAAAACCA	ACAAAGAAGC	CTTTTTAAGG	300
GTTTATAAAA	TCCCAGAGAG	CATGCCCCATA	GAAAAACGAG	AAAGTTTAAG	CAAGGTTTCT	360
AAAATCTTTT	TAGCGTTGCT	TTTTTTCATT	TCTAGCATGC	TTTTTGGGAT	CTTTTGGCGT	420
TTGCCCAAAC	GATTGGACAC	TAAATGAGT	TTAGAGAGCG	CGCACAAAAA	CGAATTAGAA	480
AATGCATTCC	AACGATACGA	TGCGCTAGGG	GTGCGTTTTG	AAGACATTGC	AGGGGTGAAT	540
GAACTCAAAG	AAGAATTACT	AGAAGTGATA	GATTATTTAA	AAAAACCC		588

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010

ATGAAACCAT	TGCATTTTTC	ACACCTGGAC	AGAGAGCAAT	CAGGCGATGT	GGGTTTTATC	60
ATTAAAAACC	TTATTTTTTT	AGGGGTTTTT	TCCTTATTGG	GTTGGTTGAA	TACCGAGTAT	120
TTTCTATGGC	CTAGCATGCT	GGAATTAAAA	AAAATCCTTT	TAGAAGAAAA	TCGTAAAAAA	180
AGCGTTTTAG	AATACGCGCA	AAGGCATTTT	GAAACAGCCC	TAGCAAATA	CCGCAATCAA	240
AAAGAAACCA	GCGAATCTTT	GTTAAAGATT	TTTAATGATG	AAGAGTCCAG	GCGGATTTTA	300
GAAAAGATCT	TAAAAAATG	TTTTGACGCC	TATAAAATCA	AACCCTTGCT	CTCTCAAAC	360
CCCTCCCAAA	AAACCCAATT	TTTTATCATG	GCTAGAGCGA	GCGAATTGGA	AAAAACTTAT	420
CTTTTTTTCA	CCTTAATCAA	CAAGTATTTA	CCGAGCGCTC	AAAGCCAATT	GCCCTTAAAG	480
ATTTCTAAAG	ATAGCGACGG	GTTGTTGGTG	CAATTTGGCG	TGAGTATTGA	TCTCCAA	537

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011

TTTAAAAGGT	ATTTTATAAC	GATGAAAATT	TTTGGGACTG	ATGGCGTGAG	GGGTAAAGCA	60
GGGGTGAAAC	TCACCCCAT	GTTTGTGATG	CGTTTAGGCA	TTGCTGCCGG	ATTGTATTTT	120
AAAAACATT	CTCAAACGAA	TAAAAATCTA	ATCGGTAAAG	ACACCAGAAA	GAGCGGCTAT	180
ATGGTAGAAA	ACGCTTTAGT	GAGCGCTCTC	ACTTCCATAG	GCTATAATGT	GATCCAAATA	240
GGGCCTATGC	CTACCCCTGC	GATCGCTTTT	TTAACCGAAG	ACATGCGCTG	TGATGCGGGC	300
ATTATGATAA	GCGCGAGCCA	CAACCCTTTT	GAAGACAATG	GCATCAAGTT	TTTCAATTCC	360
TATGTTTATA	AACTCAAAGA	AGAAGAAGAA	AGAGCGATTG	AAGAAATCTT	TCATGATGAA	420
GAATTACTGC	ATTCTAGCTA	TAAAGTGGGC	GAGAGCGTCG	GTAGCGCTAA	AAGGATAGAC	480
GATGTGATAG	GGCGCTATAT	CGCGCATTTG	AAGCACTCTT	TCCCCAAACA	TTTGAATTTA	540
CAAAAATTAA	GGATCGTGCT	AGATACGGCT	AATGGCGCGG	CTTATAAGGT	GGCTCCGGTC	600
GTTTTTAGCG	AGCTTGGGGC	TGATGTTTTA	GTGATCAATG	ATGAGCCTAA	TGGGTGTAAC	660
ATTAATGAGC	AATGCGGGGC	TTTACACCCT	AACCAATTGA	GCCAGGAAGT	GAAAAAATAC	720
CGTGCGGATA	TAGGCTTTGC	TTTTGATGGC	GATGCCGATA	GGCTAGTGCT	GGCGGATAAT	780
TTAGGGAATA	TCGTGCATGG	GGATAAGCTT	TTAGGGGTGT	TAGGGGTTTA	TCAAAAATCT	840
AAAAACGCC	TTTCTTCTCA	AGCGGTGTC	GCTACGAGCA	TGAGCAATTT	AGCCCTTAAA	900
GAATACCTGA	AATCCCAAGA	TTTAGAATTG	AAGCATTGCG	CGATTGGGGA	TAAGTTTGTG	960
AGCGAATGCA	TGCGATTGAA	TAAAGCCAAT	TTTGGGGGCG	AGCAAAGCGG	GCATATCATT	1020
TTTAGCGATT	ACGCTAAAAC	GGGCGATGGT	TTGGTGTGCG	CTTTGCAAGT	GAGCGCGTTA	1080
GTGTTAGAAA	GCAAGCTTGT	AAGCTCTATT	CGGTTAAACC	CCTTTGAAGT	ATACCCCAA	1140
AGCCTAGTGA	ATTTGAATAT	CCAAAAAAG	CCCCCTTTAG	AAAGCCTGAA	AGGTTATAGC	1200
GCTCTTTTAA	AAGAAATAGA	CCAACTAGAG	ATCCGCCATT	TGATCCGTGA	TAGCGGCACT	1260
GAAAACAAAT	TACGAATCCT	TTTAGAAGCT	AAAGACGAAA	AACTTTTAGA	ATCCAAAATG	1320
CAAGAATTAA	AAGAATTTTT	TGAAGGCGAG	TTGTGC			1356

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012

AATCATCAGC	GAATACGAAG	CCGCCAACAA	TTTAGAAAAGC	CGTTTGATCC	CTTTAGAAGA	60
GCAAGCGAGT	TAAAAGTGCG	ATCTTGCAAA	CAGATTTTTG	ATAAGGGTTT	AAAGCCCTAT	120
TATAAACATT	CTGTTTGCTT	AAAGCCTTTT	TTTAGGTTTT	GTTTCTCTCA	AATTCATGCT	180
TATCAACAGC	GTTATAGAGC	GTTTGCTCTA	ACGCTCTTTT	CTTGTAAGTT	TTTTAACGCT	240
TGTAAGATT	TTATTCCTAT	AATTGATTTT	AAAATCGTTT	TTATCCCTAT	TCTAAAACAC	300
CAAGCCAAGC	TAAAAGAGT	CTCTAATGCC	TAT			333

SUBSTITUTE SHEET (RULE 26)

748

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013

AAGCGCATGA	AAGAATCTTT	TTACATAGAG	GGAATGACTT	GCACGGCGTG	TTCTAGCGGG	60
ATTGAACGCT	CTTTAGGACG	TAAAAGTTTT	GTGAAAAAAA	TAGAAGTGAG	CCTTTTAAAT	120
AAGAGCGCTA	ACATTGAATT	TAACGAAAAA	GAAACCAATT	TAGACGAAAT	TTTTAAACTC	180
ATTGAAAAAC	TGGGTTATAG	CCCTAAAAAA	ACTCTAGCAG	AAGAAAAAAA	AGAATTTTTT	240
AGCCCTAATG	TTAAATTAGC	GTTGGCGGTT	ATTTTCACGC	TTTTTGTTGT	GTATCTTTCT	300
ATGGGGGCGA	TGCTTAGCCC	TAGCCTTTTA	CCTGAAAGCT	TGCTTACGAT	TAACCATCAT	360
AGTAATTTTT	TAAACGCTTG	CTTACAGCTT	ATAGGCGCGC	TCATTGTCAT	GCATTTGGGG	420
AGGGATTTTT	ACATTCAAGG	GTTTAAAGCC	TTATGGCACA	GACAACCCAA	CATGAGCAGC	480
CTTATCGCCA	TAGGCACAAG	TGCTGCCTTA	ATTTACAGCT	GTGGCAATTG	TATTTGGTTT	540
ATACCAATCA	TTATACCGAT	CAGTGGTCTT	ATGGGCATTA	TTATTTTGAA	AGCGTGTGCG	600

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014

AAAGAGTCTC	TAATGCCTAT	TAACCCTCTC	TATCTTTTCC	CCAATCTTTT	TACCGCTAGC	60
AGTATTTTTT	TAGGCATGAT	GAGTATTTTT	TACGCTTCCA	GTTACCAATT	TGTCATGGCG	120
TGTTGGTTAG	TGTTGGCGAG	TCTTATTTTA	GATGGGCTTG	ATGGGCGTGT	CGCAAGGCTT	180
ACCAACACCA	CTAGCAAGTT	TGGTATTGAA	TTTGACTCTT	TAGCTGATGT	GGTCGCTTTT	240
GGAGTCGCCC	CAAGCCTTAT	TACTTACTTT	TATGTGGGGT	ATAACTTTGG	GCCTATAGGC	300
ATGGCGGTGA	GCGCGTTGTT	TGTGATTTTT	GGAGCGATAC	GATTAGCGCG	ATTCAATATC	360
AGCACCAACA	CAAGCGATCC	CTATTCTTTC	ATCGGTATCC	CCATTCCTGC	GGCGGCGGTA	420

SUBSTITUTE SHEET (RULE 26)

749

TTGGTGGTGC	TTTGCCTGTT	ATTAGATAAT	AAATACCATT	TCTTAGAAGG	CAATACCGAA	480
AAGTTATTTT	TAGGCTTTAT	TGTCTTATTA	GGGGTGCTTA	TGGTGAGCAA	TATCCGCTAC	540
CCTAATTTTA	AAAAAGTCAA	GTGGAATCTC	AAGCTTTTCA	TCTTAGTGTT	GATCTTTTTA	600
TCGTTAGTGT	TTGTGCGCCC	TTTAGAGGCT	TTGAGCGTGT	TTATGGGGTT	GTATTTGATC	660
TATGGCATCA	TTGCGTGGAT	CTTTTAAATG	GTAAAAATTA	CTTTTAATAA	AAATAAAAGC	720
GCA						723

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015

TATTTGCCCG	CAAGCGAAAA	CGCCCCCTTG	CCCTCTAGTG	TTTTTAGTTC	AATCGTGGCT	60
TTGAGCTTGA	AAATAGACAG	CCTGTTTTCT	CTTTTAGCG	TGGGTAAAAT	CCCTAGCGGA	120
TCTAAAGATC	CCTTTGCGTT	AAGGCGTTTG	AGTTTGGGC	TATTGAAAAT	CATCGCGCAT	180
TACGGGTTAG	AATTTGATTT	GAAAGCGGAT	TTAAAAACC	TCTTTGAAAA	AGTGGGCGTT	240
TATCAAAGCT	TTGATTAGA	GGTTTAGAA	AAGTTTTAC	TGGAGCGCTT	TCATAATTTA	300
ATAGATTGTA	ACCTCTCTAT	TATAAGAAGT	GTGTTAAACA	CCAACGAGCG	AGACATTGTT	360
AAAAATCATT	CAAAAGTCAA	AGCCTTAAAA	CGCTTTTGT	ACAATCCTAA	GAACGCTCAA	420
AAAAAAGAGT	TGCTTTTGT	CGCTTTTCAA	CGATTAGCTA	ATATCAATAA	AGACAGAAAC	480
CCTAACGAAT	CAAGCGGGTT	TTCTACGAGT	CTTTTCAAAG	AATTACAAGA	GCATGCCCTT	540
TTTGAAGCGT	TCAACGCGAT	CAAAACAAGC	ACTTTTGAGA	GTTTGGATAG	CAAAATAGAG	600
GCTTATTTTG	GTTTGCATGC	GCCTTTAGAA	GAATATTTTA	AAAGCGTGCT	AGTCATGGAT	660
AAAGATATAG	AAATCCAAAA	AAATCGTAAA	AATTTCTTGT	GGGGCGTGTA	TCAAAGTTTC	720
TTAGAGATTG	GGGATATTAA	AGAAATTGCG	ATT			753

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

750

(B) LOCATION 1...1782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016

GTGGTCTTTA	AAATTTTAAG	TTTATGGTTA	GGGGTGTTTT	GTTTCCTTAG	GGCTACGCAT	60
TTTACTTAG	GCGAAGAACC	CAATATAAA	GACAATTTCA	CGCATTTTGA	ATACGCTAAC	120
CCTAACGCTA	GAAAAGGCGG	TGTTTGGAGA	AATGACGCTA	TAGGGACTTT	TGATAGCCTT	180
AACCCCTTTG	CGCTTAAAGG	CACTAAAGCC	GAAGGCTTGG	ATCTCATTTA	TGACACTTTA	240
ATGGTGCAAA	GCTTAGACGA	ACCTTTTGCA	GAATACCCCT	TAATCGCTAA	AGACGCCGAA	300
GTGGCTAAGG	ATAACAGCTA	TGTGATTTTT	ACCCTAGATA	AAAGAGCGAG	ATTGAGCAAT	360
AACGCTCCCA	TTTTCAGCGG	CGATGTGAAG	TTTAGCTTTG	ATACGATAAT	GAAATTAGGA	420
TCGCCCCCTT	ATAGGCAGTA	TTACCAAGAT	GTTAAAAAGG	CGGTTATCTT	AGACAAGCAC	480
CATGTTAAAT	TCATTTTCAA	AACCACTGAA	AATAAAGAAT	TGCCCCCTCAT	TTTAGGCGAG	540
TTGCAGATCT	TTTCCAAAAA	AGCGTTTCAA	AAGGATTATT	TTGAAAAAAA	CCCTTTACTC	600
ATTCTGTGTT	CTAGTGGCCC	TTATGTGATC	GCTTCTTTTG	ATGTGGGCAA	GAAAATCACC	660
TACCAAGAA	ACCCTAATA	TTGGGCGAAA	AATTTGCCTA	GCAGAAAGGG	GCAATTCAAT	720
TTTGATCAAA	TCAAATTTGA	GTATTACAAA	GATGAAACCG	TCGCCTTACA	GGCTTTTTTA	780
AGCGGGGCGT	ATGATTGGCG	CCTTGAAAGC	ACGGCTAAGG	TTTGGGCTAG	GGGCTATGTG	840
GGGAAAGCTA	TGGATAATAA	AAAAATCACT	AAATACCTCA	TAGCCCAACA	AATGCCAAGC	900
GGCATGCAAG	GGTTTTTCTT	CAACACGCGC	CGAGAAATTT	TCAAGGATAA	AAGGGTGCCT	960
GAAGCCTTAT	TTTATGCGTT	TGATTTTGAA	TGGGCGAATA	AAAATTTGTT	TTTTTCGCAA	1020
TACAAGCGCA	CCACTAGTTT	TTTCAGTAAC	TCTATCTATG	CGTCCCTTCC	TCTCCCAAGC	1080
CCTGAAGAAA	AAGCCCTGCT	AGCCCTTAT	GAAAAGAGTT	TGGATGAAAG	GGTTTTTAAA	1140
GAGCCTTATA	TCGTGCCTAG	AACCGATGGG	CCTGATGTTT	TAGGCTATAA	TTTGAGGGAA	1200
AATTTAAAT	ACGCCCAAAA	GCTTTTAGAG	AGCGCGGGCT	TTTCCTACAA	AAACATGCGT	1260
TTGGTGGATA	AGAATAACAA	GCCTTTCAGT	TTCACTTTGC	TTTTAAACAG	CCCGGCATT	1320
GAAAGACTGG	CCCTAGCTTT	TGCTAAAAAC	TTAAGGGTGT	TAGGGATTGA	AATGAAAATC	1380
CAAAGAGTGG	ATTTAAGCCA	GTATGTCAAT	CGGATCAAAA	GCTATGATTT	TGACATGATT	1440
GTAGGAGTGA	TTGGCCAATC	GTCTTTCCCA	GGTAATGAGC	AGCGCTTTTA	TTTTGGCTCT	1500
TTGAGCGCGA	AAGCCAAAGG	CACAAGGAAT	TATGCGCGAA	TCTCTAGTAA	AGCGGTAGAT	1560
GATTTGATTG	AAAGAAATCAT	TCACGCTAAA	GATTATAAGG	AGCAATTGGC	CGCCATTCAA	1620
GCGATGGATA	GGGTGTTGTT	GCGGGGGTTT	TACGCGATAC	CGCATTTTTA	TTTGCCTAAT	1680
TACAGGATCG	CAGCGTATAA	TTACATTGGC	ATGCCTGAAA	TCAGCCCTAG	CTATGGATT	1740
TCGCCGTATT	TATGGTGGAT	AAAAAAGAA	AGGGGTCTTA	AA		1782

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017

TCGTGATTG	GTGCTATAT	CATTCTTTA	AAAGAAAGTC	AAAGGCGTTT	GGATACTGAA	60
AAACTCGTTT	TAGAATCCAA	TGAAAAATTT	AAAGGCCGTT	GCGTTTTCCA	AATCTTTGAC	120
GCCATTAGCC	CCAAACATCA	AGATTTTGAA	AAATFACTTC	AAGAGCTTTA	TAACGCTCAA	180
AGTTTATGTC	AACTCTGATT	GTATCATTCT	TATGTTGGCG	CTGGTTTGAC	TTTGCCTGAA	240
TTGGGGTGTT	ATTTAAGCCA	TTATCTTTTA	TGGAAGAAT	GCGTCAAATT	AGATCAACCG	300
GTGCTTATT	TAGAAGATGA	TGTAACGCTA	GAGTCTCATT	TCATGCAAGC	CTTAGAAGAT	360

SUBSTITUTE SHEET (RULE 26)

751

TGTTTGAAAA	CCCCTTTTGA	TTTTGTGAGA	CTCTATGGGT	GTTATTGGTA	TTACCAAGAG	420
ACAAAATTCC	ATGTTTTGCC	CAAAGAATTT	GTATTTCCTC	CCTTTGATCA	TTCTTTTAAG	480
AATAACCTTA	TTTTAGAAAA	ATTTAAAAAA	TTTTTTGATG	TTTCTAGATT	TTTAAATCTT	540
TCTACCCATA	AAGTCATCCA	CCTATATTCT	CAAAAAATA	CAAAAAAGCT	ATTACGCAAC	600
GCA						603

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018

TTTAGTGAGC	GGGACTTTGA	GCTTTTTAGG	CAAAAAACAA	ACCCCTATGA	AAGATGTTCT	60
TGTGGATTG	GATTCTTGTC	AGACGCTTCA	AAAAGATCCC	TTAATCCAAC	CCTAATGATG	120
AATAATAATA	ATACCCTACC	CAAACCCCTA	GAAGAAAGCC	TAGATTTAAA	AGAGTTTATC	180
GCTCTTTTTT	AAACCTTTTT	CGCAAAAGAA	AGAGGTCTTA	TGCTTTTGA	AAACGATCTC	240
AAACAGGCTT	TCACTTATTT	AAATGAAGTG	GATGCGATCG	GTTTGCCCTG	CCCCAAAAGC	300
GTGAAAGAAA	GCGATCTTAT	TGTTGTCAAA	CTCACCAAAT	TAGGGACGCT	CCATTTAGAT	360
GAAATCTATG	AGATTGTCAA	ACGATTGCGC	TACATTGTCT	TTTTACAAA	CGCCTTTAAA	420
CCTTTCACGC	ATTTAAAAAT	TCATGAACGC	CCTAACGCCA	TTATTTTACC	CCCTTTTTTT	480
AATGATTGGA	TCCTTTTATT	GGATGATGAA	GGGCAAAATCA	AACAAGGGGC	GAACGCTACC	540
CTAGACGCTT	TGAATGAAAG	CCTGAACCGC	CCTAAAAAAG	AGAGCACTAA	AATCATTCAC	600
CATTACGCCC	ACTCTAAAGA	GCTTGCCCTT	TATTTAGTGG	ATACGCAAAG	CCACCTTAAG	660
CATGGTTATG	AATGCCTTTT	ATTAAAAAGC	GGGTTTCTTA	GCGCGATCAA	AGGCGTTGTG	720
CTAGAAAGGA	GTGCTAATGG	TTATTTCTAT	CTTTTGCCTG	AAAGCGCGCA	AAAAATCGCC	780
CAAAAAATCG	CGCAAATTGG	TAATGAAATA	GATTGCTGTA	TCGTTGAAAT	GTGCCAAACT	840
CTAAGCCGTA	GCTTGCAAAA	ACACCTTTTA	TTTTTAAAT	TCCTTTTTTA	AGAATTTGAT	900
TTTTTAGACA	GCTTGCAAGC	ACGGCTTAAT	TTCGCTAAAG	CCTACAATTT	AGAATTTGTC	960
ATGCCAAGCT	TTACGCAAAA	AAAAATGATT	TTAGAAAACT	TTTCGCACCC	CATTTTAAAA	1020
GAGCCAAAGC	CCTTAAATTT	GAAGTTTGAA	AAATCCATGC	TCGCTGTTAC	CGGCGTGAAT	1080
GCGGGCGGGA	AAACCATGCT	CTTAAATCG	CTTTTAAGCG	CAGCTTTTTT	GAGCAAGCAT	1140
CTCATTCCTA	TGAAATCAA	CGCCCATCAT	TCTACTATCC	CCTATTTTAG	AGAAATCCAC	1200
GCCATTATTA	ATGACCCCCA	AAACAGCGCG	AACAATATCT	CTACTTTTGC	AGGCAGAATG	1260
AAGCAATTTA	GCGCTCTTTT	ATCCAAAGAA	AACATGCTCT	TAGGCGTTGA	TGAAATTGAG	1320
CTAGGGACTG	ACGCTGATGA	AGCGAGCAGT	TTGTATAAAA	CCCTGTTTGA	AAAATTGCTT	1380
AAGCAAAACA	ACCAAATCGT	TATCACCACG	CACCACAAAC	GCCTGAGCGT	GTTAATGGCA	1440
GAAAACAAGG	AAGTGGAATT	ACTGGCCGCT	CTTTATGACG	AGGAAAAAGA	ACGGCCCACT	1500
TACACTTTTT	TAAAGGGGT	TATTGGCAAA	AGCTATGCGT	TTGAAACCGC	TTTGCCTAT	1560
GCGGTGCCGC	CTTTTTTGAT	TGAAAGCGA	AAGCCTTCTA	TGGCGAAGAT	AAGGAAAAAT	1620

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

752

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1365
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019

AAGCTTACCG	AGAAAATTAT	GCTTGAAACC	CCAAAAGTTT	TACTCAAAAA	CCTGCAAGAT	60
TGCAAGATCC	ATTTTCATCG	TATAGGGGGG	ATTGGCATT	CAGGCITAGC	CAAATACCTT	120
AAAGCGCAAG	GGGCTAAGAT	CAGCGGATCT	GATATTGCCA	TAAGCCCTAG	CGTTAAGTAT	180
TTGAAAGCTT	TAGGCGTAGA	AATTAATATC	CCGCATGATC	CAAAAGCGAT	CAACCATCAA	240
GATGTCATCA	TCCATTCAGC	CATTATCAAA	GAAGACAATA	CCGAAATACA	AAGGGCTAAG	300
GAATTAGAAA	TCCCTATTTT	GTCTCGTAAA	GACGCTTTGT	ATTCTATCCT	TAAAGACAAG	360
CGCGTTTITA	GCCTGTGTGG	GGCTCATGGA	AAGAGCAGTA	TCACGGCCAT	GTGAGCGCG	420
ATTTGCCCCG	CTTTTGGAGC	GATTATTGGG	GCGCATTCTA	AAGAGTTTGA	TTCCAATGTG	480
CGAGAGAGCG	CGGATATGAG	TTTGGTTTTT	GAAGCCGATG	AAAGCGATT	AAGTTTTTTA	540
TTTTCCAACC	CTTTTGGCGC	GATTGTGCCT	AACACGGAGC	CAGAACATT	GGAGCATTAT	600
GACCACGATT	TAGAACGCTT	TTTCTTCGCT	TATAAATATT	TTTTAGACCA	TGCTCAAAAA	660
AGAGTGATCT	ATAAAGAAGA	TCCTTTTTTA	AAAAACTATT	CTAAAGACGC	CATTGTTTTA	720
GAAAAAAGAG	ACATTTATAA	TATCCAATAC	ATTTTAAAG	ACGGAGAGCC	TTACACTTCG	780
TTTGAATTGA	AAAATTTGGG	GGCTTTTTTG	GTGTGGGGGT	TAGGCGAACA	TAACGCCACG	840
AATGCGAGTT	TGGCGATTTT	AAGCGCTTTA	GATGAATTAA	ATTTAGAAGA	AATTAGAAAT	900
AATTTATTGA	ATTTTAAAGG	CATTAAAAAA	CGCTTTGATA	TTTTGCAAAA	AAACGATCTC	960
ATTCTCATTG	ATGATTACGC	CCACCACCTT	ACTGAAATTG	GCACCACTTT	AAAAAGCGCT	1020
AGGATTTATG	CCAATTTATT	GAATACGCAA	GAAAAAATTA	TAGTGATCTG	GCAAGCGCAC	1080
AAATACTCTC	GCTTAATGGA	CAATTTAGAA	GAATTTAAAA	AATGTTTTTT	AGAGCATTGC	1140
GACAGGTGTA	TCATTTTACC	CGTTTATAGC	GCGAGTGAAG	TTAAAGAGA	CATTGATTTC	1200
AAAGCCCATT	TTAAGCATT	TAACCCACC	TTTATAGACA	GGGTCCGTAA	AAAGGGGGAT	1260
TTTTTAGAGC	TGTTAGTCAA	TGATAATGTG	GTAGAAACGA	TTGAAAAAGG	CTTTGTGATA	1320
GGCTTTGGAG	CGGGGATAT	TACCTATCAG	TTGAGAGGCG	AAATG		1365

(2) INFORMATION FOR SEQ ID NO:1020:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020

SUBSTITUTE SHEET (RULE 26)

753

GCGGTAACCG CCATTTTAGG GTGGGACGAA GAGGGCAAGC TCAAGTTTGG GAAAAACAGG	60
CACAAATATT TAGAAACGAG CAACGTGAAT GCCGGGAACG CCCTAACCAA TCTCATTTTA	120
ATGCAAAGAG GCTATTCTAT GAACGCTAGA GCCTTTGGCG CGGGCGATGA CATGATCAAA	180
GAAGCCATTA GCTTGAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021

AAGCTACATC GTGGATCCCA AAAACAAAAC CCTATCAATG ATCCTACTTG GGAAATTGTC	60
GGCTTTTGATT CAGCCACGCA CAAAATGAAA TCCGCCCCCA TGACTTTGGA TTTTAAGGGC	120
AATAAACTCA CCTATTCTTT GGATAAGAGC GAAAACATGA TTCTAACCAA ATTGTTCTAC	180
CAAGACTCTA AACTCTTAAA AACGAGTCAA GAACGCAAGC CTAGGGGCAT TTTTAGAGAC	240
ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG	300
GTCGCTCGCA TCGGTATTTT AGCTTTCACT AACGATCAAG GCTTAAGGAA AATCGGCGGT	360
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGCGGTAAC	420
CGCCATTTTA GGGTGGGACG AAGAGGGCAA GCTCAAGTTT GGGAAAATCA GGCACAAATA	480
TTAGAAAACG AGCAACGTGA ATGCCGGGAA CGCCCTAACC AATCTCATT TAATGCAAAG	540
AGGCTATTCT ATGAACGC	558

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022

TGGATGTTTG TAGTTAAAT GGTGTTAGGG TTTTGTATCC TTTTAAGCCC TTTGTGCGCT	60
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SUBSTITUTE SHEET (RULE 26)

754

ACTGGATTGG	ATATTTTACA	AACAGACATT	ATAGAGCGTT	CTTTAAATTT	CCCTCTGTTT	120
GTGGGGATTT	TGTGGTATTT	TTTGGCTAAA	AGATTGCGTT	CATTTTTCGA	TTCCAAAAGC	180
CTTGAATCT	CCAAACGCTT	AGAAGAGATT	CAAGCCCAAC	TTAAAGTGAG	TAAAGACAT	240
AAGAAAAAAC	TCCTTAAAGA	ATTAGAGCAA	GCCAAAGAAA	AAGCTGAATT	GATTATTTCT	300
GATGCGAATA	AAGAAGCCTA	CACGATCAG	CAAAAATACG	AATTACAAAC	CAAAATGGAT	360
GTGGAATTT	TGATCAAAAA	TTCTAAGGCG	TTGATGGATT	TAGAAGTTAA	AAAGATCAAA	420
AGAGAGTTGG	TTGAAAGCGT	TTTTAAAGAT	CTAAGAGAGA	GTAAAAAAGT	GTCCTTCAAT	480
GCGCAAGATT	GCGTGAATAT	TTTGAAACAA	AGGCTT			516

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023

ATGCAAAAAA	GTATATTCAA	AATAACTCTG	TTGTTGGTTT	TCCTCTTTTT	AAGGAATGCT	60
GTTGGTTTAG	ACGATAAAAA	AGCAGCTCCT	AAAAGCGTTC	AAAATACCCC	TAAAAATTTA	120
CCCCCTATCC	AGTTAAGGCT	CGATCAAGCC	TATGAAGACC	TTATCAAAAT	GTTAGACAAT	180
ATGGGAAAAA	GCACGCAGTA	TGAGTTCCTT	AAAATTAAAG	AAATCCTAGA	ACAAAGCGAA	240
GAGGAATGGC	TAGGAGTCGC	CCATGAAGAA	TGTGTGGCGT	TAGTCATGTT	AATAAGCCCT	300
AAGGCTTCTA	TTGAAAACAG	CCCGATTTAT	AAGAATTGCT	ATGAAGCTTA	TGTGAAACAA	360
AGAATCCATG	ATTTATATGA	TTTTTATATA	GAGGGCAAAA	AAGTGAAAAG	AAAAATCAAG	420
AAAGCCCATG	AGCATGAAAT	GGCCCTCAAC	AAATCCCAAC	CCTTAAAAAA	GGAACCGCCT	480
AAAAGCGAGA	ATAAAAAGGG	CTTAACAAAA	CCTAGCTTGA	AAGACGCAAA	GATCCCTAAA	540
GGGTATTACT	TGCAAATTGG	GGCTTTTTTA	AATTGCCCCA	GTAAGGATTT	TTTGCAAACG	600
CTCAAAACTT	TCCCTCACCA	AATGGAGGAA	AAAGACTCCC	TCACGCATTA	TTTGATTGGC	660
CCTTATAAAA	CCAAAGAAGA	AGCCCTAAAA	CAGCTTGAAA	ATGCGGCTAA	AAGCTTTAAA	720
AATAAGCCTG	CGTTGGTAGA	GAAG				744

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

755

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024

```

AGTGGATGCT ATTTTGAATC CAACTCTGAT GTGTATGTGG TTATCATTGG CTGGGCCGAT      60
CAAAAAATTG GCGTGATCGT GGATTATTTG ATCGGTCAAG AAGAAGTGGT CATCAAGTCT      120
TTAGGTTATT ATCTTAAAAA CACTAGAGGC ATTGCTGGCG CTACGGTGAG GGGCGATGGG      180
AAAATCACTC TCATTGTAGA TGTGGGGGCG ATGATGGAAA TGGCAAAGAG CATTAAGTC      240
AATATCACTA CCTTGATGAA CGAGTCAGAA AACACGAAAA GCAAAAATTC TCCTAGCGAT      300
TATGTTGTCT TGGCGATTGA TGACAGCAGC ACGGACAGAG CGATTATCCG CAAATGTTTA      360
AAACCATTAG GCATCACGCT CTTAGAGGCC ACTAACGGCT TAGAGGGCTT AGAAATGCTC      420
AAAAATGGCG ATAAGATTCC GGCAGCTATT TTAGTGGATA TTGAGATGCC TAAAATGGAT      480
GGCTACACTT TCGCCTCTGA AGTGCCTAAA TACAATAAAT TCAAAAACCT GCCCTTGATC      540
GCCGTTACCA GTCGGGTAAC TAAAACGGAC AGAATGCGCG GCGTTGAATC CGGCATGACT      600
GAATACATCA CCAAACCTTA TAGCGGTGAA TATTTAACCA CCGTAGTGAA GCGCAGCATT      660
AAATTAGAAG GAGACCAATC G

```

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025

```

ATGACCCTTT CACAAGCCCT AAATAAGGCC AAAAAAGAAT TATCGCCAAA AGGCTTTAGG      60
GGGGGGTTAG AGTCTGAAAT TTTATTAGGC TTTGTCTTGC AAAAAGAAAG GGTTTTTTTG      120
CACACGCATG AGCATTTGGA ATTAAGCCAC GAAGAAGAAA CACGCTTTTT TGAATTGGTA      180
GGAAAGCGTT TGAATGACTG CCCCATAGAG TATTATTAG GAAGCTGTGA TTTTATGGG      240
CGCTCTTTTT TCGTGAATGA GCATGTTTTA ATCCACGGC CTGAAACCGA GATTTTAGTC      300
CAAAAAGCCC TTAATATTAT TTCTCAATAC CATTTAAAAG AAATAGGCCA AATCGGCATA      360
GGGAGCGGAT GCGTGTCGCT GAGTTTGGCT TTAGAAAACC CTAATCTCTC TATTTATGCG      420
AGCGATATTT CACCAAAAGC TTAGAAGTG GCGTTAAAAA ATATTGAACG CTTTGTCTA      480
AAAGAGCGTG TTTTTTTAAA ACAACGCGC CTTTGGGATC ATATGCCAAC GATAGAAATG      540
CTTGCTCTTA ACCCGCCCTA TATCGCTAGA AATTATCCTT TGGAAAAATC CGTTCTCAA      600
GAACCGCACG AAGCCCTTTT TGGGGGGGTT AAAGGCGATG AAATCTTAA AGAAATCGTT      660
TTTTTAGCCG CTAAATTAAA AATCCCTTTT TTGGTTTGTG AAATGGGGTA TGACCAGTTA      720
AAGAGCTTGA AAGAATGCTT GGAGTTTTGC GGTATGATG CAGAGTTTTA CAAGGATTTG      780
AGCGGCTTTG ATAGAGGGTT TGTGGCGGTT TAAAAAGTT TTTTAAGA      828

```

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

756

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026

AAAGCCGTGT	TGTTCAACCC	ACTACCAACA	AAAAGGTCCG	TCATGCCCCA	TTCTTTAAAA	60
AAGCGTTTTT	TAATCGTTTA	TACCCTTTCT	ACCTTGCTTT	TAGTGGGGGT	TTGTTAGCG	120
TTGTTTTTCT	TTTATGCGAA	AAATAACCTT	TTGAAAACA	CCCAAATACG	CATGCAATAC	180
ACCGTGATG	CGATCGCTAA	AAGCCTTTTA	GAATTAAATA	ATGCCTCTTC	TTTAGAGCCT	240
TTAAAATCT	TAGAAGAAG	ATTCAAAAAC	ACCCCTTTTG	TTTTGTTGGA	CGCAGACAAC	300
AGAGTCAAGT	TTTCTAATAT	CGGGGTGTTT	GTGGCCTCTT	TTAAAAATGA	CGCCTTAATC	360
AAAACCCCTT	ATTTTGGCGT	TAAAAACAG	GGCTTTTACC	TCACAGACAG	CGCCCCAACT	420
AACCGCTTAG	GGGTTTCTAA	AATCATTATT	GCAGAAGAAG	AAATTCAAAA	AATCTTTATC	480
CCCCTTTATA	AAATGATAGG	CTATGTGTTT	TTGGGCGCGA	GTTTGTGTTG	CGCGCTAATA	540
GCCATGTGGC	TTTATAAAAT	CCCA				564

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027

AATATGCTTG	ATATATGGAT	AGATATGATA	ATCTGTATTT	TTTATTTGCT	CTTTTTTACG	60
ACTCCTTACA	TTGTAGCGGA	TATTTTGCAA	TTGAAATTTA	TCCGTCAAAA	ACTCTGCCAG	120
AAGCCTGTTT	TACTCCCACA	AAAGGATTAT	GAAGAAGCGG	GAAATTATGC	TATTAGGAAA	180
ATGCAATTAT	CCATTATTTT	TCAAATTTTA	GATGGGGTGA	TCTTTGCTGG	TTGGGTCTTT	240
TTTGGTTTGA	CGCATTTAGA	AGATCTCAGC	CATTATTTAA	ACCTTCCTGA	AACGCTAGGT	300
TACTTGGTGT	TTGCCTTGTT	GTTTTTAGCG	ATTCAAAGCG	TTTTAGCTTT	ACCCATTAGC	360
TACTATACTA	CCATGCATTT	GGATAAGGAA	TTTGGCTTTT	CTAAGGTGAG	TTTATCGTTG	420
TTTTTTAAGG	ATTTTTTCAA	AGGATTATTG	CTCACTTTAG	GCGTGGGGTT	GTTGTTGATT	480
TACACTCTCA	TAATGATCAT	TGAACATGTC	GAGCATTGGG	AGATCAGCTC	GTTTTTTGTC	540
GTGTTTGTTT	TCATGATTTT	GGCTAATCTT	TTTTACCCTA	AAATCGCCCA	GCTTTTCAAC	600
CAATTCACCC	CCTTGAATAA	TAGGGATTTA	GAAAGTCAAA	TTGAGAGCAT	GATGGATAAG	660
GTGGGTTTTA	AATCTCAAGG	CATCTTTGTG	ATGGACGCTA	GCAAGAGGGA	TGGGCGTTTG	720
AACGCGTATT	TTGGAGGCTT	GGGTAAAAAC	AAGCGGGTGG	TGTTGTTTGA	CACTTTGATC	780

SUBSTITUTE SHEET (RULE 26)

757

TCTAAAGTTG	GGACAGAAGG	GCTTTTAGCC	ATTTTAGGGC	ATGAGTTAGG	GCATTTTAAA	840
AATAAGGATT	TGTGAAAAA	TTTAGGGATT	ATGGGAGGCT	TGCTCGCTCT	TGTTTTTGCT	900
TTGATCGCTC	ATTGCCCGCC	GTTGGTTTTT	GAAGGCTTTA	ATGTCTCGCA	AACGCCAGCG	960
AGTTTGATCA	CGATTCTACT	CTTGTTTTTG	CCGGTGTTTT	CCTTTTACGC	CATGCCTTTG	1020
ATTGGGTTTT	TTAGCCGCAA	GAACGAATAC	AATGCCGACA	AGTTTGGGGC	GAGTTTAAGC	1080
TCTAAAGAGA	CTTTAGCCAA	AGCGTTAGTG	TCCATTGTGA	ATGAAAATAA	AGCGTTCCCC	1140
TATTTCGCACC	CTTTTATGT	TTTCTTGCAT	TTCACGCACC	CGCCGCTATT	AGAACGCCTA	1200
AAAGCTTTGG	ATTATGAAAT	TGAA				1224

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028

ATTAGAAGGA	GACCAATCGT	GAGCAATCAA	TTAAAAGATT	TATTTGAAAG	ACAAAAAGAA	60
GCTAATGCAA	GCTCTAAACA	AGAAGACAAT	GAAGAAATTT	TGCAATTCAT	TGGCTTTATT	120
ATTGGCGATG	AAGAATACGC	CATTCCCATT	TTGAATATTT	TAGAGATCGT	CAAACCCATT	180
GGCTACACGC	GAGTCCCTGA	AACCCCAAAC	TATGTGCTTG	GCGTGTTCAA	TTTAAGGGGC	240
AATGTCTTCC	CTTTGATCAG	TTTGCGTTTA	AAGTTTGGCT	TGAAAGCCGA	AAAACAAAAC	300
AAAGACACTC	GTTATTGGT	GGTACGCCAT	AACGATCGAT	CGCTGGGTTT	TTTCATCGCTT	360
TCTGGACTGA	TGCCATCCGA	ATCAGCATCC	ACTATTGACC	CGTCGCAGAA	ACTGTGCGCG	420
ATAACAATAA	TT					432

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029

SUBSTITUTE SHEET (RULE 26)

758

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TCGTTCTCTA TCAATAGTTT TAAAAAGGCA AAGGGAATGA AATCTACAAG AATTGGTTCT      60
AAAATTGTCA TGATGGTGTG TGCGGTTGTT ATTGTCATTA GCGCTGTTAT GGGCGTTATT      120
ATCAGCTACA AGGTGAAAG CGTGTGCAA AGCCAAGCCA CAGAATTGCT GCAAAAAAAA      180
GCTCAGTTAG TCAGTTTAA AATTCAAGGC ATTATGAAGC GCATTTTTAT GGGCGCTAAC      240
ACCCTTGAAA GGTTTTAAAG CGATGAAAT GCGCTATTA ATGACACCCT AAAAGACGC      300
ATGCTCTCTG AGTTTTGTT AGCAAACCT CATGTGTTAT TGGTTAGCGC GATTTATACG      360
AATAATAATG AACGAATGAT CACTGCAATG AACATGGATT CAAAAATCGC CTACCCTAAT      420
ACCGCACTCA ATGAAAACAT GACCAACCAA ATCCATTTCG TCAAAAGTAT AACCCGTTCA      480
GATCCCTATT ATAAAGAGGT TAATGGCGAT AAAATCTATG GCATGGACAT TACCCTCCCC      540
CTAATGGGCA AGAATCAAAA TGTTATAGGC GCGCTGAATT TCTTTTTAAA CATTGACGCT      600
TTTTATACTG ATGTGGTAGG CAAGAAAAAG AGCAACACCT TTTTAATGGG GAAAGACGGC      660
AGGATTTTAA TCAACCCTAA TCGTGAGATT CAAGATAAGA TTTTAAGCGC TATCAATCCG      720
GATAAAAGAG TCGCTAAAGC TGTGGAGTAT TACAATCAAA ACGAAGCGGG CACTTTGAGC      780
TACCATTCAT TGAGCGGGA TACAGAAACC TTTTATGCCA TACAGCCCTT TGATTTTTTT      840
GAAGAAAAAG GGAATAACGG CCAATCATTG GCGTTGGGCA ATTGGGAAAT ATGTCAA      897

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(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030

```

GGGGTATTTT ACAATAGCTC TCTCCACAG CCCCCAACTA AAAACCCCTT AACCCGAGAA      60
TACCGCTTTT TAAAGAGATT ATCACTTATT TATGCAAGCT CTTTATTGTT ATTTATTTTA      120
AAAAATGCCC TTAAGCTTTT TTTAATTTTG TTAATCATGC TTAATAAGCC AAAGCCTTTA      180
TTTTTGCTCT TGGTTAAGCC TTTCTTCTAT CTTTTTGATT TGGTGGCTCA TTTGAGCACT      240
CGCATTGATT TGATTGATAA GCATGTAAAG GTTTATCATC ATCAAAAGCA CCACCACAAG      300
CCC                                                                303

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(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

759

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031

TTTATCACTG	GGATAGAAAT	CCACCCGGGC	GCTAAGATTG	GGAGAGGGCT	TTTTATTGAT	60
CATGGCATGG	GTGTGGTGAT	TGGCGAGACC	ACAGAGATTG	GAGATGATGT	TACCATTAT	120
CATGGCGTAA	CTCTGGGGGG	TACGGGCAAG	TTTAAGGGCA	AACGCCACCC	TACTTTAGGC	180
AACCGAGTGG	TAGTTGGGGC	AGGGGCTAAG	GTCTTGGGCG	CGATTTGCGT	GGGCGATGAT	240
GTGAGGATTG	GGGCTAATGC	GGTGGTGCTT	TCAGATTAC	CCACGGGTTC	TACGGCTGTA	300
GGTGCTAAAG	CCAAAACCAT	CACAAAGGAT	CGT			333

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032

AAAGGTTTTT	TAGGTGTTAA	AAAAGTTATT	GTTTTTATTA	AAAAAAGGG	TGAGATGGTC	60
GTCAACTCCA	AAGTGCAAAC	GCTTAAAGTC	TTTTCAAAAT	TTTTCAGCAA	TTTCAAAATC	120
ACTAAACTCA	AAGACAACCA	CGAAGAAGCC	CACAAACTTT	TTGGAGAAAA	TAGCCGTAAA	180
GCCCATGACA	CTGAGATCAT	TTACTCCACT	TTGCAAGTGG	TCCCCAGGTA	TTCAATAGAA	240
ACCGTGGGCT	TTAGTTTGTT	GATTTTAGCG	GTCGCTTACA	TCTTATTCAA	ATACGGCGAA	300
GCTAGAAATG	TACTCCCTAC	CATTTCTATG	TATGCCCTAG	CGCTTTATCG	CATACTCCCT	360
TCTGTAACCTG	GAGTGATCAG	CTATTATAAT	GAAATCGCTT	ACAACCAGCT	TGCAACCAAT	420
GTGTGTTTTA	AAAGCCTTTC	TAAGACCATC	GTTGAAGAGG	ATTTAGTCCC	TTTAGACTTT	480
AATGAAAAAA	TACTCTCCA	AAACATTTCA	TTGCTTATA	AGTCAAAACA	CCCGGTTTTA	540
AAAAATTTCA	ACCTCACCAT	TCAAAAAGGT	CAAAAAATCG	CTCTCATAGG	CCATAGCGGG	600
TGCGGAAAAAT	CCACGCTGGC	GGATATTATT	ATGGGGCTTA	CCTACCCTAA	AAGTGGGGAA	660
ATTTTTATTG	ATAACACCCT	TTTAACCAGC	GAAACAGGC	GCTCATGGCG	TAAAAAATA	720
GGCTATATCC	CCCAAATAT	TTACCTTTTT	GATGGCACTG	TGGGGGATAA	TATCGCTTTT	780
GGGAGTGCTA	TAGATGAAAA	ACGCTTGATT	AAGGTGTGCA	AAATGGCTCA	TATCTATGAT	840
TTTTTATGCG	AGCATGAGGG	CCTTAAAACC	CAAGTGGGCG	AAGGGGGCGC	TAAGCTTAGC	900
GGCGGTCAAA	AACAGCGCAT	AGGCATCGCA	AGAGCCTTAT	ACGATAACCC	TGAAATTTTG	960
GTTTTAGATG	AAGCCACTTC	AGCCCTAGAC	AATGAAACCG	AGAGTAAAT	CATGGATGAA	1020
ATCTATCAAA	TCGCTAAAAA	TAAACCCTA	ATCGTTATCG	CCCACCGCTT	AAGCAGGATT	1080
GAACGCTGTG	AAGTCATCAT	TGACATGAGC	CAACACAAAG	ACAATCTCGG	C	1131

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

760

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033

```

GCCTATAAAA AAGGGGAAAT CATGGCGCTT GAAGTGGTTT TATGGGATTT TGATGGCGTG      60
ATTTTGTACA GCATGCATTT AAAATATGAA GGGTTTAAGG CGTTGTTTCA AAAGCATGGC      120
AACGATAGTA AAGAGGGTTT GAAACAATTT GAAGTTTATC ACTATCAAAG TGGGGGGATT      180
TCAAGGAATG AAAAGATCCA ATATTTTTAT AACGAGATTT TAAAAACCCC TATCGCTCAA      240
GAAGAAATAG ATGCATTAGC CCTAGAGTTT GCGCGTATCA TAGAGCAAAA GCTTTTTGAT      300
AGGGGGGCATT TGAATAGCGA AGTGATGGCG TTTATTGATA AGCATTATCA AAATTATATT      360
TTCCATATCG CTTCAGCGGC CTTCATAGC GAATTGCAAG TGTGTGCGA GTTTTTAGGG      420
ATTACTAAGT ATTTTAAGAG CGTTGAAGGG AGTCCGCCTG ATAAACCCAA GATTATCGCT      480
AATATCATTC AAAAATACGC CTATGACCCA AGCCGTATGC TAATGATAGG CGATAGCGTC      540
AATGATTATG AAAGCGCTAA GGCTAATAAA GTGGCGTTTT TGGGCTATAA CAGCAAGGTT      600
TTGAAAAAAT TAGTGGGGCA AGATGGCTAT CAAGGGAAGT ATTTGGAGAG CTTTAAGGGG      660
TTTGATTTAC AAAACTTCGC AAAAGAG

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(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034

```

AATAAAGCA TGCAGCATTT AGTCTTAATC GGTTTTATGG GGAGCGGTAA AAGCTCTCTA      60
GCACAAGAAT TGGGGCTGGC TTTGAAATTA GAAGTGCTGG ATACGGATAT GATCATTAGC      120
GAGAGGGTGG GCTTGAGCGT GAGAGGGATT TTTGAAGAGC TTGGCGAAGA CAATTTTCAGG      180
ATGTTTGAAA AAAATTTGAT TGATGAATTA AAAACGCTCA AAACCCCCA TATCATTCT      240
ACCGGTGGGG GCATTGTGAT GCATGAAAAT CTTAAGGGTT TAGGCACAAC TTTTACCTC      300
AAAATGGATT TTGAGACCTT GATTAAGCGT TTGAATCAAA AAGAAAGGGA AAAACGCCCC      360
CTTTTGAATA ACCTCACTCA AGCCAAAGAG CTTTTTGAAA AACGACAAGC CCTCTATGAA      420
AAAAACGCTT CCTTTATCAT TGATGCAAGG GGTGTTTAA ATAATTCTTT AAAACAAGTG      480
CTACAATTCA TCGCA

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SUBSTITUTE SHEET (RULE 26)

761

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035

```
ATTTTTTTTA AAGGCCTTGT GATGTTAAGT AGAGACATTG TCCAATATTG CAAGATCCGC      60
ACCGAGTTAT ACGCCTACCT CACTTATTTG TTTTCGCACA ATATCCGCAA CCACCTTCCT      120
GAAATCACTT TGGATTATTT AAACAGGCAA ATCAGTAAGA TGCAAGCTGA AATCAAAATG      180
GCAAAAAGTT TTTTGTGTTT AGACGCTAAG GGCATGCTCA TGCTTAAGCC AAGCCAATTT      240
AAAGAGCAGG GGCATAAGGA AGGGCTATTA GAGCATGATT TAACAGAAGG GATTGAATTA      300
GAATCGCATG TCAGTTTTAG CGATAAGTAT TATTTTTATC AAGCCGTGAA TGAAAAGCGT      360
TGCATTTTAA CCGACCCCTA TCCTTCTAAA AAAGGGAACC ATTGGTAGT GAGCGCGTCT      420
TACCCGGTGT ATGATCAAAA TAACGATCTA GCGTTTGTGG TGTGCTTGCA AATCCCTTTG      480
AGGGTGCGCA TTGAAATCAG CTCGCCTTCA AAGTATTTA AAACCTTTAG CGAAGGGAGC      540
ATGGTCAATG ATTTTATGAT TTCTATCATG CTCACCTTAG TGTGCTGCT TTTATTCGTG      600
AAATGCATTT CTAGCTTTTG GACAGCGATC GTGCATTTA GCAGTTTTGA CATTAAAGAA      660
GTGTTCCACC CCATTGTGCT TTTAACCCCTA GCTTTAGCCA CCTTTGATTT GGTCAAGGCG      720
ATTTTGAAG AAGAAGTGTT GGGTAAAAAT AGCGGGGACA ACCACCATGC GATCCACCGC      780
ACCATGATCA GGTTTTTAGG CTCTATCATT ATCGCATTAG CCATTGAAGC GTTAATGCTC      840
GTGTTTAAAT TCAGCGTGAG CGAGCCGGAT AAAATCACTT ATGCGGTGTA TTTGGCTATC      900
GGCGTGCGCG TGCTTTTGAT CAGTTTGGCG ATTTATGTTA AATTCGCTTA TAGCGTGTTC      960
CCCAAACGAG AACGC
```

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036

SUBSTITUTE SHEET (RULE 26)

762

GAGAGTTATC	AAACGGTATT	TACACGCCAG	AGGTATTATC	AGCGGTTGTT	TAGACGAGCT	60
GTTCGTAGGA	ACCTGCGCGT	CTGTGAGTTC	ACAAATCAAA	ATAACAAGAG	GGGTGATTGT	120
CAACGTCAGC	AGTAGCTTTT	CTATGGGGCT	TACCATGGCG	AGTGCTTATG	ATCCCATTTC	180
AGGATCGCAA	AAACCCATTG	TGGGGCAAGC	CCTTTTATTG	TAGCGATTT	TAATTTTATT	240
GGATTTATCG	TTCCACCATC	AAATCATTTT	ATTTGTGGAT	CACAGCTTAA	AAGCCGTCCC	300
TTTAGGGCGA	TTTGTCTTTG	AGCCAGAATT	AGCTAAAAAC	ATTGTCAAAG	CCTTTTCACA	360
CTGTGTTGTC	ATAGGGTTTT	CTATGGCGTT	CCCTATTTTA	TGCTTGGTGT	TATTGAGCGA	420
TATTATTTTT	GGCATGATCA	TGAAAACCCA	CCCTCAATTC	AACCTGCTCG	CTATCGGGTT	480
TCCGGTTAAA	ATTGCGATCG	GGTTTGTGGG	CATTATTTTA	ATCGCTTCGG	CTATCATGGG	540
GCCTTTTAAA	GAAGAAATCA	GCCTGGCCTT	TAGCGTTATT	AGTAAATCT	TT	592

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037

GGGGTTTTGC	GTTCCTCTAT	CTTTTTTAAA	GTTGTCGCTT	TGTTTATGAT	AACGCTCTTT	60
AGTTTTGGAG	CGTTCGCTTA	CTATTTCTGT	TCTTCTCAAA	TCAGTCACGA	AAACTATCAA	120
AACGAAATGC	GCCATTACCA	GTTTGTTACC	ACTATCAATG	AAATTTTAAA	TAACACTCT	180
GATTATAGAG	CCATAGAAGA	TTACCTCTAT	AAAATTGGCT	TTAGAGAAAC	CACAATAGAA	240
AATTTAGAAA	AGGTTTTAGC	CAAAAGACGC	CACCAGTTGC	ACCACAGAAA	TATTTGGTAT	300
GCTGAAGTGT	TTAAATTCAG	CGATATGGTT	TTTATCCTTT	TAAAAAAGGA	TGAGCATTTT	360
GTGCTTTATA	AAGATTGCA	TTCGGTTTCT	TATAGGAATT	ATTTCTTAGC	CATTACGGTG	420
GGTTTATAT	TGATTTTATT	CCTCTTTTTA	TTTGTTTTGC	AGAGTTTATT	GCCTTTAAGA	480
GAGTTAAGAT	CTCAAGTGAA	ACGCTTCGCT	CAAGGGGATA	AAAGCGTGAG	TTGTAAAAGC	540
AAGCAAAAAG	ATGAAATAGG	GGATTTGGCT	AACGAATTTG	ACAATTGCAT	CCAAAAAATC	600
AATGCGATGA	ATGAATCTCG	GGTTTTATTT	TTGCGCTCTA	TCATGCATGA	ATTACGCACC	660
CCTATCACTA	AGGGCAAGAT	ACTAAGCTCT	ATGCTCAAAG	AAGAGCTGTC	TTGCAAAACG	720
TTTTCATCTA	TATTTGATCA	CTTGAACATG	TTGATTGAGC	AATTTGCCCC	CATTGAGCAG	780
CTCGCTTCCA	AAAATTATGG	GAGCAATAAA	GAAAAATTTT	TAATGAGCGA	TTTGATAGAT	840
AAGATTGAAA	AAATGCTTTT	AATTGATGAA	GATAAAAAAA	GCCCTATCCA	TGTATCCTCT	900
TCAAATTACA	TCATTGAAGC	GGATTTTGAA	TTGTTTGCTA	TAGCGTTAAA	AAACATGATA	960
GACAATCGCA	TCAAATACAG	CGATGACAAA	CAGGTGTTTT	TGGATTTTAT	AGGGAATAAT	1020
TTAGTGGTGT	CCAATAAAAG	CAAACCTTTA	AAAGAAGATT	TTGAAAAGTA	TTTGCAACCC	1080
TACTTTTAAAT	CTTCTAACCC	CAGCCAAGCC	CATGGGTTTG	GGTTAGGCAT	GTATATCATT	1140
AAAAACGCTT	TAGAGGCTAT	GGGATTGAAT	TTGAGCTATC	ATTATAGCAA	TGGAAGAATC	1200
TGTTTCACTA	TCCATGATTG	CGTTTTTAAT	AGTTTTTACG	ATTTAGAAGC	GGATAATGAA	1260
GAGCTACCCC	CCCCCGAAA	ATTTGAGAGA	GGTGAAGGGA	ATGAAGGGAA	CAGAAAAAGC	1320
CAATTGTGGG	GT					1332

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

763

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038

AGAAAAACAA	AAAGAGAGAA	CATGTTCAAA	CGATTGAGAA	GATTACGAAG	CAGCGAAAAT	60
TTAAGAGCGA	TGGTGAGAGA	AACACGTTTA	AATATTAATG	ATTTTCATCGC	TCCCTTATTT	120
GTCATAGAAA	GCGATAGCGG	TATTAAAAAC	GAAATCAGCT	CCATGCCTGG	CGTGTATCAA	180
ATGAGTATAG	AGCCTCTTTT	AAAAGAATGC	GAAGAATTAG	TGGGTTTAGG	CATAAAAGCC	240
GTTTTATGCT	TTGGCATTTC	TAAACATAAG	GACGCTACAG	GAAGCCATGC	GTTAAATAAG	300
GATCACATTG	TCGCAAAAGC	TACGAGAGAA	ATTAAAAAAC	GATTTAAGGA	TTTGATCGTT	360
ATAGCGGATT	TGTGTTTTTG	CGAATACACC	GACCATGGGC	ATGCGGGGAT	TTTAGAAAAC	420
GCTTCTGTGT	CTAACGATAA	AACGCTAAAG	ATTTTAAATC	TTCAAGGGCT	TATTTTGGCT	480
GAAAGCGGTG	TGGATATTCT	AGCTCCAAGC	AACATGATGG	ATGGCAATGT	TTTAAGCTTG	540
AGAAAAGCAC	TGGATAAGGC	CGGGTATTTT	CACACGCCCA	TCATGAGTTA	TTCCACTAAA	600
TTTGCGAGCA	GTTATTACGG	GCCTTTTAGA	GATGTAGCCA	ATTCTCCGCC	GAGTTTGGC	660
GATCGCAAAA	GCTATCAAAT	GGATTACGCT	AACCAAAAAG	AAGCGCTTTT	AGAAAGCTTG	720
GAAGATGAAA	AACAGGGTGC	GGATATTTTA	ATGGTGAAGC	CGGCTTTAGC	GTATCTGGAT	780
ATTGTTAAAG	AAATCAGAGA	TCACACTTTG	CTCCCTTTAG	CGCTCTATAA	TGTGAGTGGG	840
GAATACGCCA	TGCTCAAAC	CGCTCAAAAA	CACAACCTGA	TCAACTATGA	AAGCGTTTTA	900
TTAGAAACGA	TGACTTGTTT	TAAAAGAGCG	GGAGCGGATA	TGATTATTAG	CTATCATGCT	960
AAAGAAGTGG	CTAATTATT	ACAAAGGAAT				990

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039

AGCGCAGGGC	GCAATTTGGC	AGAGGATATT	ATTTGCGTTC	ACGCTTTGCC	TAAATTCAAT	60
CAAAGCGCTA	TGGACGGCTA	TGGGTTTAAA	ATGCAAGACT	TGGGCCAAAA	AACTCAAGTT	120
ATCCAACACA	TCTTTGCCCG	GGATGATGTG	AGCGCTTTAG	AAGTCAAAGA	AAATGAATGC	180
GTTAAATCA	TGACTGGAGC	GATGGTGCCA	AAGGGAATAG	AAACGATCGT	TCCCATAGAA	240
TGCATGCTAG	AGAGTCATAA	AGATTTCGCC	CTAGCTCCTA	AAGATTTTAA	AATTCACGCT	300

SUBSTITUTE SHEET (RULE 26)

764

AATATCCGTC	AAAAGGGCGA	GAACGCTTCT	TTAAACAGCG	TTTAGTCCC	TAAAAATACC	360
CGTTTGAATT	ATGGCCATAT	CGCGCTCATT	GCCTCTCAAG	GGTTCAAAGA	AATCAAAGCG	420
TTTAGAAAAT	TAAAAATCGC	TCTCTTAGT	AGCGGCGATG	AATTAGTGCC	TTTAGGGCAA	480
AACGCCCTAG	AGTGCCAGGT	TTATGATGTT	AATTCAGTGG	GTGTTTTTAA	CATGCTTAAA	540
AACACAACA	CGCATTTTCT	AGGGGTTTTA	AAAGATGATA	AAAATTTACA	GCTTAAAATA	600
CTTGAATTGC	AAGGCTATGA	TGTCATCCTT	TCAAGTGCGG	GGGTGAGCGT	AGGGGATAAA	660
GACTTTTTTA	AAGACGCTTT	GAAAGAAAAG	AACGCCCTTT	TTTATTACGA	AAAAGTCAAT	720
CTCAAACCTG	GAAAGCCGGT	AACTTTAGCC	CAACTCAATC	AAAGCATTAT	TATAGGCTTA	780
CCGGGTAATC	CTTTAAGTTG	CTTACTGGTT	TTACGAGTTT	TGATTCTACC	CTTATTGGAG	840
CGCTTATCCT	TAAATAAAGA	TTTTAAATTA	AAACCCTTTA	AGGCTCAAAT	CAATGCCCCCT	900
TTAAAGCTTA	ATAACAAACG	GACGCATTTA	ATCTTAGGCA	ACTATTCAAA	CCACCAATTC	960
ATTCCTTACA	ACAACCGCTA	TGAATCAGGA	GCGATTCAAG	CCCTTGCGCA	AGTGGATTCT	1020
ATCGCTTTAA	TTGATGAAGG	AGTGGGATTG	GTCAGGGCG	AAATTGAAAT	TTTAAGGTTT	1080
GAAAAAT						1086

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040

GGGAATTACG	GCCTAGAGAT	TAGATTTAAG	GAAATGGCAG	TGTTAAAAAA	GATGATAGGT	60
TTGGTGGCGG	TTTTAAGCGT	TTTATTAGCC	AGAGACAACC	CTTTTGAGCC	TGAAATCAAT	120
TCCAAGAATT	TGCAAGGGGG	CTTTAGCGGG	ATCTATGATG	ACTACCTCAA	AGAAATCCAT	180
GTGGATTTCG	CCACGAGCGC	TAGGATCTTA	AAAAAAATCA	CGCTCACTTA	CCAAGATATT	240
GATGGCTCTA	TCCATTCTAA	AGTCGTGGGT	ATTGATAAAA	GCATTGATTG	GCACTACCCC	300
TTAAAACTTT	CCCAACACAC	CCTTAATCAA	GACGCCTTTG	AAAAACGCTA	CCAGATCCAA	360
GATTTTGATT	TTTTAATGGC	AAACAACACG	ATGATTTTGC	GTTCCCCCTTA	TAAAATTTTG	420
CGCTCTTTTG	TGTTAGTCAA	TCCTTATAGA	ATCGTGTTAG	ACACGCAAAA	AGGCCCTTTG	480
GATATTTATC	AAAACATGGA	TTTAAACCAG	AAGTTTTTTT	CTCACATTAA	AGTCGGCACC	540
CACAAAGATT	ATTACCGCAT	CACGCTCATT	TTAGACGGGA	AATACCGCTA	TCTTTTGGAA	600
GAAAAAACG	GGGCGTATGA	ATTAAACTG	AAA			633

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

765

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041

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AAAGCAGTGG CTACGCCTCA CCACACCCCC TTATGGCTCA GCGTGTATGA AAGCTTTAAA      60
GAAGCCCTAG ACTTTAAGGA AGTCATTCTA GTTGTAGCG AATTGGATTA TGTATTATATT      120
CAACGCCATT ACCCCAAAAT CAAGCTTGTA AAAGGCGGGG CATCAAGGCA AGAATCCGTG      180
CGTAACGCTT TGAAAGTAAT TGATAGCACT TACACGATCA CCAGCGATGT GGCTAGGGGT      240
TTAGCGAATA TGAAGCGCT TAAAAGCTTG TTTTAAACC TCCAACAAAC GAGCCATTAT      300
TGCATCGCCC CTTACTTGCC TTGCTATGAC ACAGCGATCT ATTATAACGA GGCTTTAGAT      360
AGAGAAGCGA TCAAACTCAT TCAAACCCCG CAATTAAGCC ACACCAAAAC GCTCCAATCA      420
GCCCTAAACC AAGGGGGTTT TAAAGATGAA AGCAGCGCGA TTTTACAAGC TTTCCCTAAC      480
TCTGTGAGCT ATATTGAAGG CAGTAAGGAT TTGCACAAAC TCACCACAAG CGGCGATTTA      540
AAGTTTTTTA CGCCTTTTTT TAACCCAGCA AAGGACACTT TTATAGGCAT GGGTTTTGAT      600
ACGCATGCGT TCATTAAAGA TAAGCCTATG GTTTTAGGGG GGGTTGTTTT GGATTGCGAG      660
TTTGGGTTAA AGGCTCATAG CGATGGCGAT GCTTTATTGC ATGCGGTTAT TGATGCGATT      720
TTAGGAGCGA TTAAGGGGGG GGATATTGGC GAATGGTTCC CTGATAATGA CCCCAAATAC      780
AAAAACGCCT CTCTAAAGA GCTTTTAAAA ATCGTGTGGG ATTTTCTCA AAGCATTGGG      840
TTGAATGTC TTGAATGGG AGCGACCATC TTTAGCGAAA TCCCTAAAAT CACTCCTTAC      900
AAACCGGCGA TTTTAGAGAA TTTGAGCCAA CTTTGGGTT TAGAAAAATC TCAAATCAGC      960
TTGAAAGTCA CTACAATGGA AAAAAAGGG TTCATTGGCA AACAAGAAGG GCTGTTAGTC     1020
CAAGCGCATG TGACATGCG TTATAAACAA AAACCT                                     1056

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(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042

```

TGCTTGGGGA TGTGTTTTAT TCTAAAGCCT TTTTGTAGTT GTCTAAAATG GGCGAATCCA      60
TCGCTCAAGC CCCTCTCTAA TGCAGTTTTA AGGCTCTCTA GGGGCGAGAT TGAAGACGTG      120
TTTGTGGGGG AATGTTTTAA TAGCGACAAA CAAAATACT GGCCTATTTT AGAAGACAAG      180
ACCGCCCAT TCATAGAAGC GAGCTGAAA AGCATGGCGA TTCTTTTAAA TAAAGACGCC      240
AAAATGTATG CGGATTTTGG GTTGCATTTT GGCATGGCGT TTCAAATCAT TGATGATTG      300
TTAGACATCA CTCAAGACGC CAACACTCTA GGTAAAGCCA ATTTTAGCGA TTTTAAAGAG      360
GGCAAGACCA CTCTACCTTA CTTGCTTTTA TATGAAAAAT TGAATCAGCA TGAACAAGGG      420
CTTTTAATT CCTATTTC AACAAGATAG CATGAAATCA TAGAATGGAC TAAGGAAAAA      480
TTCAAGCAAC ATGGTATCAT AGAAGAAACC CTTAAAATCG CTCAAGTTTA TTCTAAAAAG      540
GCCCTGAAG CCATTAAAGG GGAAAACAAT TTGATTTTAG AAAAAGTAGC GCAAGATGTC      600
ATTTATAGGA CTTT                                     615

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SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043

AAGAAGGTAA AGATGAATAT CAAAATTTTA AAAATATTAG TTGGAGGGTT ATTTTTTTTG	60
AGCTTGAACG CCCATTATG GGGGAAACAA GACAATAGCT TTTTAGGGAT TGGTGAAAGA	120
GCCTATAAAA GCGGGAATTA TTCTAAAGCG GCGTCTTATT TTA AAAAAGC ATGCAACGAT	180
GGGGTGAGTG AAGGCTGCAC GCAATTAGGA ATCATTTATG AAAACGGGCA AGGCACTAGA	240
ATAGATTATA AAAAAGCCCT AGAATATTAT AAAACCGCAT GCCAGGCTGA TGATAGGGAA	300
GGGTGTTTTG GCTTAGGGGG GCTTTATGAT GAGGGTTTAG GCACGGCTCA AAATTATCAA	360
GAAGCCATTG ACGCTTACGC AAGGCATGCG TTT	393

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044

TCCAGCAAAA CAGCATTTCAG GGCAAGCAA ATCATCACCG CAACCGATAT TAGCGCTCAA	60
AAACGCCAAG AGCGGCTCGC TTCTATGGGG AAAATTTCAG CGCATTTCAG CCATGAAATC	120
AGAAACCCCG TAGGCTCTAT CTCTCTTTTA GCTTCGGTGT TATTAAAGCA TGCGAACGAA	180
AAAACATAAC CCATTGTTGT AGAATTGCAA AAAGCTTTAT GGCGCGTAGA AAGGATCATT	240
AAAGCCACCT TGCTTTTTTC TAAAGGCATT CAAGCCAACC GCACCAAGCA AAGTTTGAAA	300
ACGCTAGAGA GCGATCTCAA AGAAGCCCTA AACTGCTACA CTTACTCTAA AGACATTGAT	360
TTTCTTTTTA ATTTTAGCGA TGAAGAAGGG TTTTGTGACT TTGATTTAAT GGGGATTGTG	420
TTACAAAATT TCTTGATATA CGCCATTGAT GCGATTGAAG CCTTAGAAGA GAGCGAACAA	480
GGTCAGGTCA AAATTGAAGC GTTCATTCAA AATGAATTTA TTGTCTTCAC CATTATTGAT	540

SUBSTITUTE SHEET (RULE 26)

767

AATGGCAAGG	AAGTGGAAAA	TAAAAGCGCT	TTATTTGAGC	CTTTTGAAAC	CACTAAATTA	600
AAGGGGAATG	GCTTAGGGTT	AGCCCTGTCT	TTGCAAGTCG	TTAAAGCCCA	TGAAGGGAGC	660
ATTGCGCTAT	TAGAAAATCA	AGAAAAAACC	TTTGAAATTA	AGATTCTTAA	CGCTTCT	717

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045

AAGCCTAAAA	CAATTTTAAA	AAAAGGACTT	TTGATGAAAA	CATTTGAAAT	TTTAAAACAT	60
TTGCAAGCGG	ATGCGATCGT	GTTATTTATG	AAAGTGCATA	ACTTCCATTG	GAATGTGAAA	120
GGCACCGATT	TTTTCATGT	GCATAAGCC	ACTGAAGAAA	TTTATGAAGG	GTTTGCGGAC	180
ATGTTTGATG	ATCTCGCTGA	AAGGATCGTT	CAATTAGGAC	ACCACCCCT	AGTCACTTTA	240
TCCGAAGCGA	TCAAACCTAC	TCGTGTTAAA	GAAGAACTA	AAACGAGCTT	CCACTCTAAA	300
GACATCTTTA	AAGAAATCT	AGAGGACTAC	AAACACCTAG	AAAAAGAATT	TAAAGAGCTC	360
TCTAACACCG	CCGAAAAAGA	AGGCGATAAA	GTTACCGTAA	CTTATGCGGA	CGATCAATTA	420
GCCAAGTTGC	AAAAATCCAT	TTGGATGCTA	GAAGCCCAT	TAGCT		465

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046

GGAATTTGCA	TGCAAGAAAA	ACGACTTAAA	GCCATTCAAA	ACAAAATCGC	TTCTTGGATC	60
AAGGAAATTG	AAAGCGGCTT	TATAGATGCA	TTGTTTCTA	AGATTGGCCC	TTCAAAGATG	120
CTGCGCTCCA	AACTCATGCT	CGCTTTGTTA	GACGAAAAAA	CAGACGCTAT	TTTATTAGAT	180
AAAGCGCTCA	ATTTGTGTGC	GATTGTGGAA	ATGATACAGA	CCGCTTCTTT	ATTGCATGAT	240

SUBSTITUTE SHEET (RULE 26)

768

GATGTGATTG ACAAGGCGAC CATGCGCCGA AAGCTCCCTA GCATTAACGC TCTTTTTGGG	300
AAATTTTAACG CCGTGATGCT TGGGGATGTG TTTTATTCTA AAGCCTTTTT TGAGTTGTCT	360
AAAATGGGCG AATCCATCGC TCAAGCCCCT CTC	393

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047

TCGATGCTAT TTTCAAACT TTTGCCCCA ACGCTCAAAG AACCCCAAA AGACGCCGTG	60
TTAAAAAGCC CTAAGCACCC CGGGAACGGG GGACACCCCC TTCAAATAGG CAGTGGGATT	120
TATAATTTC TACCCCTAGC TAAAAAAGTG CTAGACAAAA TAGAAAACGT CACGCACAAA	180
CGCATGCAAG AGCATGGGGC GCAAAATATT TTAATGAGTT TTGTGTTTT GCGGAGTTTG	240
TGGGAAAAAT CAGGCCGTTT GGATAAATAC GGCAAGGAAT TATTGGTTTT TAAAGACCGA	300
AAAGACAATG ATTTTGTTTT AAGTCCCCTT TTAGAAGAAA ATATCACCGA AATTGCCGCT	360
AATTTTCATCA AAAGCTACAA GCAATTACCC GTGCATCTCT ATCAAATCCA CACGAAATTC	420
CGTGATGAAA TCCGCCCAAG ATTCCGGTTG GTGAGAGCGA GGGAAATTTAT CATGAAAGAT	480
GGTTATAGCT TTCTAGAAAG CGCTGAAAGC TTGGATAAGG AAATTTTAAA CACGCAAAGC	540
GCTTATAAAG AGATTTTAAAG CGATTTGGGT TTGGATTTTC GCATGTGTGA AGCGGATAGC	600
GGGGCGATTG GGGGGAGTAA AAGCAGGGAA TTTGTCGTTT TAACAGAATG CCGGGAAGAC	660
ACGATCGTGG TGTGTCAAAA TTGCGATTAT GCCGCCAATA TTGAAATCGC TAAACGCTCT	720
AAAAGAAGCT AGCCTTTAAT GTCCCAAGC GCATTAGCGA AATTCCTCAC CCTAATACC	780
ACCAGCGCTC CAAGCGTGGC GGAGTTTTTT AAAACAGAGC CTTATTTTGT CTTAAAAGCG	840
CTTGTTAACA AAGTGATCCA TAAAGATAAA GAAACCCTAG CGTGCTTTTT TGTTAGGGGC	900
GATGACAATT TAGAAGAGAC TAAAGCCCTA AACACTTTGA ATCTTTTGGG GCGGAACGCT	960
TTAGAATTAA GAGAGGCCAA TGAAGAAGAT TTAATAAAG CAGGGTTAAT AGCGGCTTT	1020
ATAGGGCCTT ATGGCTTGAA AAAGCATGTT TGTTATATTA TTTTGTATGA AGATTTAAAA	1080
GAGGGCGATT GCTTGATCGT TGGGGCTAAT GAAAAGGATT TTCATGCGGT GGGCGTGGAT	1140
TTAAAAGGGT TTGAAACCT TGTTTATGCG GATATGTCC AGGTTAAAGA GAGCGATTGT	1200
TGCCCTAATT GTCAAGGAGC GTTGAAATAC CATAAGAGTT TGGAAGTGGG GCATATTTTC	1260
AAACTCGGGC AAAGCTATGC TAAAAGCTTG AAGGCTAGTT TCTTGATATA GAATGGCAAA	1320
GAGCGGTTTT TTGAAATGGG GTGCTATGGG ATAGGCATTA GCCGGTTGCT CAGCGTGATT	1380
TTAGAGCAAA AAAGCGATGA TCTAGGCTGT GTGTGGACGA AAAATACCGC TCCTTTTGAT	1440
GTGGTGATCG TGGTTTCTAA CCTGAAAGAT GAAGCGCAAA AAAAATCTGC TTTTGAAGTG	1500
TATGAAAGAC TGCTCCAAAA GGGCGTTGAT GCGCTGTTAG ATGACAGAGA CGCTCGTTTT	1560
GGGGCGAAGA TGAGGGATTT TGAATTGATT GGGGAACGAT TAGCCTTGAT TGTGGGAAG	1620
CAAACTTTAG AGAGTAAGGA ATTTGAATGC ATCAAACGCG CTAATTTAGA AAAGCAAACG	1680
ATCAAAGACA TAGAATTAGA AGAAAAAATT TTAGAAATGT TAGCGAGCGA A	1731

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

769

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048

ATTCGTGAGC	CACAGGTTGC	AATAATGACT	GCAATGATGC	GTTATTTTCA	CATCTATGCG	60
ACCACTTTTT	TCTTCCCTTT	GGCGCTTCTT	TTTGCGGTTA	GTGGGCTTTC	ATTGCTCTTT	120
AAAGCGCGCC	AAGACACTGG	CGCTAAGATC	AAAGAAATGGG	TTTATAGAAA	ATCCTTAAAA	180
AAAGAAGAAC	GATTGGACTT	TTTAAAAGGC	TTTATAAAAG	AAAACCATAT	CGCTATGCCT	240
AAAAAGATAG	AGCCTAGAGA	GTATAGGGGA	GCGTTAGTCA	TTGGCACGCC	TTTGTATGAA	300
ATCAACCTTG	AACTAAAGG	CACTCAAACG	AAAATCAAGA	CCATTGAAAG	GGGCTTTTTA	360
GGCGCGCTCA	TCATGCTGCA	TAAGGCTAAG	GTGGGCATCG	TGTTTCAGGC	GCTTTTAGGG	420
ATTTTTTGCG	TGTTTTTATT	GTTGTTTTAC	TTGAGCGCGT	TTTTAATGGT	GGCTTTTAAA	480
GACACTAAAC	GCATGTTTAT	AAGCGTTTTA	ATAGGGAGCG	TGGTGTCTCT	TGGAGCGATC	540
TATTGGTCTT	TG					552

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049

CTAATAAAAA	GCAAATCAAA	AAAGTGGCTT	TTGGTAGGGG	AAGGGGCGAA	TAGTGAAATC	60
TTTGAAGCTT	CCATGCAATC	GCTTTTAAAA	ACGGATGGCG	TTTATTCTAA	CCACAAACCT	120
ATTTATCAAG	AGTTTTACGA	ACTCAATTTC	CATAACGGGT	TGTATTATCA	GCCTAATGTG	180
TTTTTTGCTT	ATGAATCTTG	CGCGTTAGGG	TTTAGAAAAG	GGGGGTAAAT	TTTGGATAAT	240
TTTTCTAAAT	TCGTAGGCCA	CAGGTTGCAA				270

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

770

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...849
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050

ATGCTAGAGA	GCGTGAACGT	TAAAATTTCT	GCAGACGATA	TTAAATCTAA	AAATGTCGCT	60
GCCGTGATGA	TTACAGCCTC	CTTGCCCCCC	TTTGCAAGAC	AGGGCGATAA	AATTGATATT	120
CACATTTCTT	CTATTGGCGA	TGCGAAATCC	ATTCAAGGAG	GGACTTTAGT	GATGACCCCT	180
TTAAATGCGG	TAGATGGGAA	TATTTACGCC	CTCGCTCAAG	GGGCTATCAT	TTCGGGTAAT	240
TCTAGTAACT	TGCTCTCAGC	CAATATCATC	AACGGGGCGA	CTATTGAAAG	GGAAGTTTCG	300
TATGATTTGT	TCCATAAAAA	CGCCATGACT	TTAAGCCTGA	AAAACCCCAA	TTTTAAAAAC	360
GCTATCCAAG	TGCAAAACAC	TTTAAATAAG	GTATTTGGTA	ATAAAGTAGC	CATAGCGCTA	420
GATCCCAAAA	CCATTCAAAT	CACCCGCCCA	GAGCGTCTTT	CTATGGTGGA	GTTTTTAGCT	480
TTAGTGCAAG	AAATCCCCAT	TTACTACCGC	GCGAAAAATA	AGATCATTTG	AGATGAAAAA	540
TCAGGCACGA	TCGTTTCAGG	AGTGGATATA	ATCGTGCATC	CTATAGTGGT	TACAAGCCAA	600
GACATCACGC	TTAAATACAC	TAAAGAGCCT	TTAAATGATT	CTAAAAACAT	GCAGGATTTA	660
GACAATAACA	TGTCCTTAGA	CACCGCTCAC	AACACGCTGA	GTTCTAACGG	GAAAAACATC	720
ACCATTGCCG	GGGTGGTAAA	AGCCTTACAA	AAAATTGGCG	TGAGCGCTAA	GGGGATGGTT	780
TCAATCTTGC	AAGCCCTAAA	AAAAAGCGGC	GCGATTAGCG	CGAAATGGAG	ATACTATGAT	840
AAACAACAA						849

(2) INFORMATION FOR SEQ ID NO:1051:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051

ACGGGACATG	GCAGGTTAGG	GTGGATATTA	AATCCAAAGA	AGGCCAAGTT	TATCGCACTA	60
AAACAAGCCT	GGATTTATGA	GCGCATGCTA	TCTTTTATAA	GCGCGTTTGA	TAAAAGGGGC	120
GTTTCAATAC	GCCTTCTAAC	AGCCTTGTTA	CTGCTTTTTA	GTTTGGGTTT	GGCTAAAGAT	180
TTAGAAATCC	AAACTTTTGT	GGCTAAATAC	CTTTCTAAAA	ATCAAAAAAT	ACAAGCCCTA	240
CAGGAGCAAA	TTGACGCTTT	AGATTCTCAA	GAAAAAGTCG	TTAGCAAAATG	GGATAACCCCT	300
ATTTTGTATT	TAGGCTATAA	CAACGCTAAC	GTGAGCGATT	TTTTCAGGCT	GGATAGCACC	360
TTAATGCAAA	ACATGAGCTT	GGTTTGTCT	CAAAAAGTGG	ATTTAAATGG	TAAAAAACTC	420
ACGCAGTCTA	AAATGATCAA	TTTAGAAAAA	CAAAAAAATA	TATTAGAGCT	TAAAAAAACC	480

SUBSTITUTE SHEET (RULE 26)

771

AAGCAGCAAT TGGTGATTAA TTTAATGATA AACGGCATTG AAAACTATAA AAACCAACAA	540
GAAATAGAGC TTTTAAACAC AGCGATTAAA AATTAGAAA ACACCCTCTA TCAAGCCAAC	600
CATTCCAGTT CGCCCGATTT AATAGCGATC GCCAAGTTAG AAATTTTAAA ATCGCAATTA	660
GAAATC	666

(2) INFORMATION FOR SEQ ID NO:1052:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052

ATTGTTTTTC ATCAAGGGAG TTTGAGCGTG AGCGGTTTGT TTAAAATGCG TATTCTGAGT	60
TTTAAAAAGA ATAAGCGGGC GGTGTTTTCA CTCTATCTTT TTATCGCTTT GTTAGCGCTT	120
TCTCTTTTAG CCCCTTTGTG GGTCAATGAT CGCCCTTTAT TCATCTATAA AGACAATAAA	180
GCGTATTTC CTATGTTTAA AAACATATGCG GAAGTGGAGT TTGGAGGCCA TTTTTCACC	240
CCTACGGACT ATAACGATCC TTATGTGCAA AACACGCTTT TAAAAGACGC TTTTCATCATC	300
CATGCGCTCA TCCCTTATAG CTACGATACG ATCATTATGG ATTTAGACTC GCCTGCCCCC	360
ACCCCCCAA GCTTCAAACA CCTTTAGGC ACAGACGATC AAGCCAGAGA CGTGTTAGCC	420
AGGCTGGTTT ATGGCTATCG GGTTCGTTA GTGTTTGGGA TTTTACTCAC CCTTTTAGC	480
GTTCTTATG GCGTGAGTTT GGGGCGGTTT CAGGGGTATT ATGGAGGGCT AGTGGATTTA	540
GTGGGGCAA GGTGAGCGA AATTGGAGC GCGATCCCCA TGCTTTTTTT ACTCATTGTG	600
ATTTCTAGCG CGTTCAATC TAATTTTGG ATCATCTGT TTTAGTCTT GCTCTTTAGC	660
TGGATGGGC TTTCTCAAGT CGTGCGCACG GAGTTTTTAA AAGCAAGGAA TATGGACTAC	720
ACCAAAGCCG CTAGAGCGCT TGGGGTGAAT GATTTAAAAA TCATTTTCTA CCATGTTTTA	780
CCCAACGCTT TAGTGGCAAC GATCACTTAC ATTCCTTTT TAATGGCGGC TAGTATTTCC	840
ACTTTAGTGT CTTTGGATT CTTAGGTTT GGCATGCCA TAGGGAGCGC GAGCTTGGGC	900
GAATTGGTCA ATCAAGGCAA GGATAACCTC ACCACGCCTC ATTTAGCGGT TGTAGCCTT	960
GTAGCCATTA GCTTGTGCT TTCTGTTTTG GTGTTTCATTG CGCAAGGGGT GCGCGATGCT	1020
TTCAACGCTA ACATGCTCAA A	1041

(2) INFORMATION FOR SEQ ID NO:1053:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

772

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053

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AGGGGTTACA TGCTAGAAAT CAAGAATTTA AACTGCGTTT TAAACTCTCA TTTTTCGCTC      60
CAAAACATCA ATATTTCCTT AAGTTATAGT GAAAGGGTGG CGATCGTGGG CGAAAGCGGG      120
AGCGGGGAAA GCTCTATCGC TAATCTCGTC ATGCGATTAA ACCCTAGATT CAAGCCCCAT      180
AATGGCGAAA TCCTGTTTGA AACAACCAAT CTTTAAAGG AAAGCGAAGC GTTCATGCAG      240
CATTTAAGGG GGAATATTAT CGCTTACATC GCCCAAGACC CCCTATCCAG CCTAAACCCC      300
TTGCATAAAA TCGGCAAGCA AATGAGTGAA GCCTATTTT TACACCATAA AAACGCTTCT      360
CAAGTGCTCC TTAAAGAACA AGTTTAAAC GCCATGAAAC AAGTCCAATT GGATGAAAAA      420
TTTTTGATC GTTACCCTTA TGAGCTCAGC GGTGGGCAAC GCCAAAGGGT GTGTATCGCT      480
ATGGGCATTA TTAACGCGCC AAAACTGCTC ATTTGCGATG AGCCTACCAC CGCGCTAGAT      540
GCGCAATCC AAAACCAGAT TTTAGACTTG CTCAAGCAAT TGAGCGTGGA AAAAAACATC      600
GCCCTTTTAT TCATTAGCCA TGATTAAAG CCGGTTAAAC GATTGGCTGA TAGGGTTTAT      660
GTGTTAAAAA AAGGCGAGAT AGTAGAAACC AATTGACTA AAGAGCTTTT TAATGACCCC      720
AAGCAGCAAT ATTCAAACT CTTGATTGAG GCTTCAAACT TGCCCCGCTAA AAATTAAAAA      780
GCGCTAGATG AGACGCTTTT AGAGGTGAAA GATTTTAGCG TTTATTACTT GCAAAAACGC      840
TTCTTTAGCG CTTCTTTAAA AAAACCCCTT ATCGCATCGG TGGATTTTTC CCTCAAAGCT      900
AAAGAAAACA TCGGCATCAT TGGCGAAAGC GGGAGCGGGA AAAGCTCTCT AGCGTTAGGG      960
CTTTTAAAC TCGCTTTAAA CAGCGGGGAA GAAAAGATT TTAGCCAAAG CGTGGGGCTT      1020
TTAAATCTA AGCGGTTCAA ACCCTACCGC AAGATTITGC AAATGGTGT TCAAGACCCC      1080
TACGCATCAT TAAACCTCG CTTAAGCATT CAAAGCATT TAATAGAAGC TTTGCGCTTT      1140
GCTTACCCTA AAGCTTCACA ACAAGAATGG CACCATTAG CTGAACCTTG CTTAGAAGAA      1200
GTGTGTTTAA ACCCTGAATT GCTTAACTTT TACGCTTATG AGCTCAGCGG AGGGGAGCGC      1260
CAAAGAGTGG CGATCGCTAG AGCGATTGCC TTAACCTA GAATCATTCT TTTAGATGAG      1320
CCAACCTCTG CTTTAGACAA AAGCATTCAA AAAAGCGTGT TGGAAATTAT GTTGAATTTA      1380
CAAGAAAAGC AGGATTGAG CTATTTGTTT ATCAGCCATG ATTTAGATGT GATCAAAGCT      1440
TTTTGCGATA GGGTGTAGT GGTGAGTGAG GGGAAAATCG TGGAAACAGG CGCTATTGAA      1500
GAGGTGTTTG ACAACCCCAA ACACGCTTAT ACCAAGCGTT TGTGGAATC CAGGCTT      1557

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(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054

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GGGGGACTTA TGAATACTAT TATAAGATAT GCGAGTTTAT GGGGCTTGTG TATTACTCTA      60
ACTCTAGCGC AAACCCCTC TAAAACCCCT GATGAAATCA AGCAAATCCT TAACAATTAT      120
AGCCATAAGA ATTTAAAGCT CATTGATCCG CCGACAAGTT CTTAGAAGC GACACCGGCT      180
TTTTTACCCT CGCTAAAGA AACAGCGACC ACGATCAATC AAGAGATCGC TAAATACCAT      240
GAAAAAAGCG ATAAAGCCGC TTTGGGGCTT TATGAATTGC TAAAGGGGGC TACCACCAAT      300
CTCAGTTTGC AAGCGCAAGA ACTCAGTGTC AAGCAAGCGA TGAAGAACCA CACCATCGCC      360
AAAGCGATGT TTTGCTTAC TTTGAACGCG AGTTATAATT TTAAAAATGA AGCTAGGGAT      420

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SUBSTITUTE SHEET (RULE 26)

ACTCCAGAAT ATAAGCATT TAACACCCAA CAACTCCAAG CTCAAGTCAC ATTGAATGTG	480
TTTAATGGCT TTAGCAATGT GAATAATGTC AAAGAAAAGT CTGCGACTAC CGATCCACTG	540
TGGCTAATT	549

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055

GTGAAATTCA GCGTTTAAAC CCTTTTCCCG CAACTCATCT TGCCTTATTT TGAAGATTCT	60
ATTTTAAAAA GAGCGTTAGA AAAAAACCTT TTTGAATTGG AAGTGTTAAA CCTTAGAGAT	120
TTTAGCGCTA ACAAATATCA AAAAGCGGAT CACACGCTCA TTGGTGGGGG TGCGGGGCAA	180
ATTTAGACC CTGAGATGAT AGAAAACGCA CTCCACTCTG TTA AAAACCC TAAACACACG	240
ATTTTTTAA GCGCGGTGGG CAAGCCTTTC AAGCAAATAG ACGCGATGCG TTTGGCTCAA	300
AAAAAGCATG TCGTTTGGT GTGCGGGCGT TATGAGGGCT TTGATGAACG CTCTATTGAA	360
TTGGGTGCTG ATGAGTTTTT TTGTATAGGC GATTTTATTT TAACAGGGGG CGAGCTTGGG	420
GCGTTGTGCT TGATAGATAG TATCGCTCGC CACATTCAAG GGGTTTGGG TAACGCCCAA	480
TCTTTAGAAA ATGAGAGTTT TGAAAATAAT TATTTGGAGA CCCCTAATTT CGCTAACGCT	540
GTTTTTAAAT CCAAAGAAAT CAATAAATC CCTGCACCTT TAGAATATTC TAAAGGAAAT	600
CATGCTAAAA TCAAGCAACT AAAGCTTGAT TTGTCAAAAT TAAGGACAAA ATTTTACCGC	660
CTTGATTTAT TCAAACAGCA CAAATCA	687

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056

774

AGGGAGCAGT	GGTTTCACTT	TCGCTCAACG	CCCCCACC	TGGTTTTAAT	GGCAGGTTTG	60
CAAGGGAGCG	GGAAGACAAC	CACCACCGCT	AAACTCGCCC	ACTATCTCAA	AACCAAAAAT	120
AAAAAAGTGC	TTTATGCGC	ATGCGATTTC	CAACGCTTAG	CAGCGGTGGA	GCAATTAAAG	180
GTTTGGGCG	AACAGGTGGG	CGTGGAAGTT	TTTCATGAAG	AAAATAAAAG	CGTGAAGAA	240
ATCGCCAACA	ACGCTTTAAA	AAGGGCTAAA	GAAGCGCAAT	TTGACGTGTT	AATCGTGGAT	300
AGCGCGGGGC	GTTTAGCGAT	TGATAAGAG	CTTATGCAAG	AATTAAAGGA	AGTTAAAGAA	360
GTCTTAAATC	CCCATGAAGT	GCTGTATGTC	GCAGACGCGT	TGAGCGGGCA	AGATGGGGTC	420
AAAAGTGCGA	ACACCTTTAA	TGAAGAAATA	GGCGTGAGCG	GGGTGGTGTT	AAGCAAATTT	480
GATAGCGATT	CTAAAGGGGG	TATCGCCTTA	GGCATCACTT	ATCAATTGGG	CTTACCCTTG	540
CGTTTTATTG	GGAGTGGGGA	AAAAATCCCT	GATTTAGACG	TGTTTATGCC	TGAAAGGATT	600
GTGGGGCGTT	TGATGGGGGC	TGAGATATT	ATCTCGCTCG	CTGAAAAAAC	CGCCAGCGTT	660
TTAAACCTTA	ATGAAGCCAA	AGATTTAAGC	AAAAAGCTCA	AAAAAGGGCA	ATTCACTTTC	720
AACGATTTTT	TAAACCAAAT	TGAAAAAGTG	AAAAAATTAG	GCTCTATGAG	TTCTCTGATC	780
TCTATGATTG	CAGGTTTAGG	GAATATGGCA	AGCGCGCTAA	AAGACACGGA	TTTAGAAAAGT	840
TCTTTAGAAG	TGAAAAAAAT	CAAGGCCATG	GTTAATTCCA	TGACGAAAAA	AGAGCGAGAA	900
AACCCCGAGA	TTTAAACCGG	CAGCCGAAGA	AAAAGGATCG	CTTTAGGGAG	CGGCTTAGAA	960
GTGTCTGAAA	TCAATCGCAT	CATCAAACGC	TTTGATCAGG	CGAGCAAAAT	GGCGAAACGA	1020
CTCACGAATC	AAAAGGGTAT	TAGCGATTTC	ATGAATCTAA	TGAGTCAGGC	TAAAAATCAA	1080
ACGCCCCCTA	AAATGCGC					1098

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057

AGGAAAGCGA	TGAACACCCA	CCTCAAACAA	TTGATTGAAA	TTTCGCACTT	GGATAAAGAA	60
ATTGACTCTT	TAGAGCCGTT	GATCAGAGAA	AAACGGAAG	ACTTGATAA	AGCCTTGAAT	120
GATAAAGAAG	CTAAAAATAA	AGCGATTTTG	AATTTGGAAG	AAGAAAAATT	AGCCCTAAAA	180
TTACAGGTTT	CTAAAAACGA	GCAAACCTTA	CAAGACACGA	ACGCTAAAAAT	CGCCAGTATC	240
CAAAAGAAAA	TGAGCGAGAT	CAAATCCGAA	AGGGAGTTGC	GCTCTTTAAA	CATTGAAGAA	300
GATATTGCTA	AAGAGCGATC	CAATCAAGCC	AACAGAGAAA	TTGAAAACCT	GCAAAATGAA	360
ATCAAGCACA	AAAGCGAAAA	ACAAGAAGTT	TTGAAAAAGG	AAATGCTAGA	GCTTGAAAAA	420
TTAGCGTTGG	AATTGGAAAA	TTTAGTGGAA	AACGAAGTCA	AAAACATCAA	AGAAACCCAA	480
CAGATCATCT	TTAAAAAGAA	AGAAGAACTC	GTGGAAAAAA	CCGAGCCTAA	AATCTATAGC	540
TTTTATGAAA	GGATTAGGAG	GTGGGCGAAA	AACACGAGCA	TCGTAACGAT	CAAAAAACAG	600
GCTTGTGGGG	GTTGTTTTAT	TCGGTTGAAC	GATAAGATTT	ATGCCGAAGT	GCTAACGAGT	660
GGGGACATGA	TCATTGTGCC	GTATTGCGGG	CGTATTTTAT	ACGCTGAGAG	TACGCATGAA	720
AGTAACGCTC	AACCTCCAAA	AGAAAGCCAA	CCAAAAGAAA	GCCAAGAAGA	AAGCCAAGAA	780
GAAAGCCAAG	AAGAAAGCCA	AGAATCCGTT				810

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1701 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

775

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058

ATGAACGAAA	TTGACAAATC	CGTTGATATC	GGATTCTTAC	GGATTCTGGA	TGTTATTAAA	60
AAAGTTAAAA	CCCCAAAGGG	TGGTATTGAG	GTTTTAAGGA	CTTTAATGA	TTTCACGCCC	120
AAAATTGAAA	ACGCCCTAAA	TTTAGCGACC	AAAAGCCATA	AGGGGCAATA	CAGAAAGAGC	180
GGTGAGCCTT	ATATTGTCCA	TCCTATTGTC	GTGGCGAGCG	TGGTGGCGTT	TTGTGGGGGC	240
GATGAGGCGA	TGTTGTGCGC	CGCGCTTTTG	CATGATGTGG	TAGAAGACAC	GCCTTGTGAG	300
ATTGAAACGA	TTGAGCGAGA	ATTTGGGCAA	GATGTGGCTA	ATTTAGTGGG	TGCGCTCACC	360
AAAATCACTG	AAATCAGGAA	AGAAGAGTTA	GGCGTGAGTT	CTCAAGATCC	CAGAATGGTG	420
GTTTCAGCCC	TCACCTTTAG	AAAGATCCTT	ATTAGCGCGA	TACAAGATCC	AAGAGCCTTA	480
GTGGTTAAAG	TTAGCGACAG	GTTGCACAAC	ATGCTCACCT	TAGACGCCTT	GCCTCATGAC	540
AAGCAGGTGC	GTATTTCTAA	AGAAACTCTA	GCGGTGTATG	CCCCCATAGC	GAGTCGATTG	600
GGCATGTCTT	CAATCAAAAA	CGAATTAGAA	GACAAGAGCT	TTTATTATAT	TTATCCAGAA	660
GAGTATAAAA	ATATTAAAGG	GTATTTGCAC	AAAAACAAAC	AGTCTTTACT	CTTAAAACTC	720
AACGCTTTTG	CGAGCAAGTT	AGAAAAAAG	CTTTTGTACA	GCGGGTTTAG	CCATTCCGGAT	780
TTTAAACTCG	TTACAAGGGT	GAAACGCCCT	TATTCTATTT	ATCTTAAGAT	GCAACGAAAA	840
GGGGCGGTTA	ATATTGATGA	AAATTTGGAC	TTGTTAGCCA	TTAGGATTTT	ATTGAAAAAC	900
CCGATTGATT	GCTACAAGGT	TTTAGGGATT	ATTCATTTGA	ATTTCAAACC	CATTGTTTCT	960
CGTTTTAAAG	ATTACATCGC	TTTGCCCAA	GAAAAATGGCT	ATAAGACAAT	ACACACGACG	1020
ATTTTTGATG	AATCTTCTGT	TTATGAAGTG	CAGATCCGCA	CTTTTGATAT	GCACATGGGG	1080
GCGGAGTATG	GTAATTCAGC	CCATTGGAAG	TATAAAGCCG	GGGGCGTGGA	TCATGAAGAA	1140
CATCATGAGG	GCATGCCGGT	GTTGCAAAAT	TTTAAATACC	ATGACAGCGA	TTTAAAAAAC	1200
GACCCTAAGG	AATTTTACGA	ACTCGCTAAG	AACGATTGTG	ATCGTGAAGA	TATTGTCTGT	1260
TTTTCGCCCC	ATGGGGACAC	TTACACTTTA	CCGGTGGGCG	CGATCGCTTT	AGATTTGCTG	1320
TACATGGTGC	ATAGTGATTT	GGCGGATAAA	GCCACGGACG	CTTATATCAA	TAGTAAAAAA	1380
GCCTTACTCA	ATCAAGAATT	AAGGAGTGGG	GATGTGGTTA	AAATCATTAA	AGGCGATAAA	1440
GTAATACCTC	GTTTCATTTG	GATGGATCAG	CTTAAAACTT	CTAAGGCTAA	AAACCATTTG	1500
CGCATCCAAA	GAAGAAACCG	CTTGAAAGAA	ATTGACACTA	AGAGCATGAT	CAATATCTTA	1560
TCGACTTTTT	TTGGGCGCTC	TGTTTTTGAA	GATGCGGATT	TGAAAGATTA	TAAAAACTTT	1620
GAAGAAAAAT	TAACAGATTG	TGGGGTGGAG	ACCACCTTAA	CAGAAGCGAT	GAAAAGCTTT	1680
GAAAATTTGG	GCCAAACTCA	C				1701

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

776

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059

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GTTACAATCA AAAGCTTTAT TAATGGATTA AGAAGGGATC ATGCAGGCAA AGATAAAAAA    60
CAAGCGGGTT TTGGTGAAAT TTTCTGGGGA AGCGTTAGCT GGGGACAACC AGTTTGGATT    120
GACATTCATG TGTTAGATCA CATCGCTAAA GAGATCAGAA GTTTAGTGGA AAACGATATT    180
GAAGTGGGTA TTGTGATTGG TGGAGGCAAT ATCATTAGGG GGGTTAGCGC GGCTCAAGGG    240
GGGATCATTG GGCGCACCAG TGGGGATTAT ATGGGCATGT TAGCCACCGT GATTAATGCG    300
GTAGCCATGC AAGAAGCTTT AGAGCATATC GGTTTAGACA CAAGAGTGCA GAGTGCCATT    360
GAAATCAAAG AGATTTGTGA AAGTTATATT TATAGGAAAG CGATCAGGCA TTTAGAAAAG    420
GGTAGGGTGG TGATTTTGGG CGCTGGCACA GGAACCCCGT TTTTCAACCAC CGATACGGCC    480
GCTACTTTAA GAGCGATTGA AATTGGATCG GATCTAATCA TTAAGCGGAC TAAAGTGGAT    540
GGCATCTATG ACAAAGACCC TAACAAATTC AAAGACGCTA AAAATTGGAC ACTT        594

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(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060

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ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA    60
AGCCCAGCGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA    120
AAAAACCGGA TTGAAAATTA CGAACACGCG ATTGAAGCCA TTAAGCTAGG AGGCGTTCCT    180
GTAGCGTATG TGGGCGATGT GGTGGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT    240
ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAAGGAG TGGAGGCATT    300
GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA    360
CCCATTGTGG CTGATGTTAA GGATTGAAA GAGGGCGATA TCATTAAAT CTACCCCTTAT    420
AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT    480
TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC    540
AATAAAGCGC GTAAATTTTT AGGGCTAGGC GAATCGGAAG CGTTCAAAAA ACCATCCGCT    600
CCTAAAAGCG ACGCTAAAGG CTACACTTTA GCCCAAAAAA TTGTAGGCCA TGCTTGTGGG    660
GTAAAAGGGA TCTTACCTGG TGCTTATTGT GAGCCAAAGG TTACCACCGT GGGCAGTCAA    720
GACACCACAG GGGCGATGAC CAGAGATGAG GTTAAAGAAT TAGCGAGTTT GAAATTTGAT    780
GCGCCTTTTG TGTTCAGAG TTTTTCGCAT ACCGCTGCTT ACCCAAAACC TAGTGATGTG    840
AGTTTGCATG CAACCTTGCC TGGCTTTATC ACTCAAAGAG GGGGCGTGGC GTTGCATCCG    900
GGCGATGGCG TGCATCATAC ATGGCTTAAT CGCATGGGAT TGCCTGACAC TTTAGGCACA    960
GGGGGGGATA GCCACACCCG TTTCCCTTTA GGCATCAGTT TCCGGCAGGG AGCGGGC    1017

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(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs

SUBSTITUTE SHEET (RULE 26)

777

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061

ACATTACTA TAAAGAGATT TGTTTTGATG AAAATTAAAA TCCAAAAAAT CCACCCAAAC	60
GCCCTTATCC CTAAATACCA AACCGAAGGC TCTTCAGGCT TTGATTGCA CGCTGTAGAA	120
GAAGTAGTGA TCAAACCTCA TAGCGTGGGA TTGGTAAGGA TTGGGATTTG TTTGTCTTTA	180
GAAGTGGGGT ATGAACTGCA GGTACGCACC CGTAGCGGCT TGGCTTTGAA TCATCAGGTG	240
ATGGTGTTAA ATTCCCCTGG CACGGTGGAT AATGATTATA GGGGCGAAAT TAAGGTCATT	300
TTAGCGAATT TGAGCGATAA AGATTTTAAA GTTCAAGTAG GGGATAGGAT CGCTCAAGGG	360
GTGGTTCAAA AAACCTATAA AGCCGAATTT ATAGAATGCG AACAATTAGA TGAAACTTCA	420
AGGGGTAGCG GGGGGTTTGG CAGCACAGGA GTGAGTAAGG CA	462

(2) INFORMATION FOR SEQ ID NO:1062:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062

AGAAAGAAAC CATTCAAGGA ACGCATTGAT TTGATGAATA AACCATTTTT AATCTTACTC	60
ATAGCCCTAA TTGCCTTTAG CGGCTGTAAC ATGAGAAAAT ACTTCAAACC CGCTAAACAC	120
CAAAATTAAAG GCGAAGCGTA TTTCCCTAAC CATTTGCAAG AAAGCATCGT TTCGTCTAAT	180
CGTTATGGAG CCATTTTGAA AAATGGAGCG GTTATAGGCG ATAAAGGTTT AACGCAGCTA	240
AGAATTGGTA AGAATTTCAA TTATGAAAGC AGTTTTTTAA ATGAGAGTCA AGGGTTTTTC	300
ATCCTTGACAC AAGATTGTTT GAACAAGATT GATAAAAAA CAAGCAAAAG CAGGGCGGCT	360
AAGACTGAAG AAACGGAATT GAAATTAAAG GGCGTTGAAG CGGAAGTCCA AGATAAAGTC	420
TGTCATCAAG TGAATTGAT TAGCAATAAC CCTAACGCCA GCCAACAATC TATCGTTATT	480
CCTTTGGAGA CTTTTCCTT GGCGCGAGCG TTAAAGGGAA TCTTT	525

(2) INFORMATION FOR SEQ ID NO:1063:

SUBSTITUTE SHEET (RULE 26)

778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063

GGCATGAGCA	TTAAGGAAAA	TTTAGAGCAA	GTTAGAAACG	AATTTAAAAG	CGATGAAAAG	60
CTTTTAGAAG	GAGCGTTTAG	ATTAGAAAAG	TTTTTCAAAC	GCTACAAGTG	GGTGTGTTG	120
TTTATCGTGG	TGGCTTTTAT	CGCTTATTTA	GGGGATACAA	AATTACAAGA	TTATAAGCAT	180
GAGCAAACGA	GAGAGCGGAT	CACTCAAATT	TATAATGAAG	TGCTAGAGAG	TCCTAATAAT	240
ATAGCCTTGC	AAAAAAGATT	GAAAGAAAGTC	GCCCCAGAGT	TGTATGACTT	GTATCAGTTC	300
GCCAGAGCGA	GTGAGAGGAA	CGATGCAAAC	GAGTTTAAAA	GGCTTTCGCA	ATCTTCTAAT	360
GAAATCGTTA	AAGCGTTCGC	CAAATATTCT	TACGCATCGC	TCTCTAGAGA	TAAAAACCTG	420
CTTGAAAAAA	GCCCCATTCT	TAAAGAAATG	AGCGCTTTAC	AAGAAGTGAA	CTTGTTGTAT	480
GAAGAAAATT	CTAAGACGCG	AATCAAAAAA	GCGCATCAAA	GTTTATCAAC	TATCCCTCTA	540
AGTTCTTCAC	TCTATGCTAT	AATCTCTGTT	TTAAAACATT	ATGGAATGTT	AGAAGATATT	600
CAGCAAAACC	CTTCCAAACC	AACCAATCTA	AAGAAAGAAA	CCATTCAAGG	AACGCAT	657

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064

AAGCGCTATA	AAAGGCTAGA	GCAAGAAATA	AAAAAAGGG	ATAAAATGAT	AGTGGGTTTG	60
ATAGGGGTTG	TGGA AAAAAT	CTCTGCTTTA	GAAGCGCATA	TAGAAGTGCA	AGGGGTTGTT	120
TATGGGGTGC	AAGTTTCTAT	GCGAACGGCT	GCTTTGCTCC	AAACGGGCCA	AAAAGCGCGT	180
TTGAAAATCT	TACAAGTGAT	TAAAGAAGAT	GCGCATCTTT	TATACGGGTT	TTTAGAAGAG	240
AGCGAAAAAA	TTCTCTTTGA	AAGGCTTTTG	AAAATCAATG	GGGTAGGGGG	GCGTATCGCT	300
TTAGCCATTC	TTTCAAGCTT	TTCCGCCAAT	GAATTTGAAA	ACATTATCGC	TACTAAAGAA	360
GTCAAAAAGAC	TCCAGCAAGT	CCCAGGCATA	GGGAAAAAGC	TCGCCGATAA	GATCATGGTG	420
GATTTGATTG	GCTTTTTCAT	TCAAGATGAA	AACAGACCCG	CGCGCAATGA	AGTCTTTTTA	480

SUBSTITUTE SHEET (RULE 26)

779

GCCCTAGAGA GTTTGGGCTT TAAAAGCGCT GAAATCAATC CAGTTTAAA AACCCCTAAAA 540
 CCCCATCTCA GCATAGAGGC AGCGATTAAA GAAGCCTTAC AGCAACTGCG CTCT 594

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065

AGTCGCACCC	TTTGTGCAAA	AATCGTTT	CAAAAAGAAA	GGAAGAAAAT	GGAAATACAA	60
CAAACACACC	GCAAAATCAA	TCGCCCTTTA	GTTCCTCTCG	TTTTCAGCAGG	AGCGTTGATT	120
AGCGCCATAC	CGCAAGAGAG	TCATGCCGCC	TTTTTCACGA	CCGTGATCAT	TCCAGCCATT	180
GTTGGGGGTA	TCGCCACAGG	CACTGCTGTA	GGAACGGTCT	CAGGGCTTCT	TAGTTGGGGA	240
CTCAACAAG	CCGAAGAAGC	GAATAAAACC	CCAGATAAAC	CCGATAAAGT	TTGGCGCATT	300
CAAGCAGGAA	AAGGCTTTAA	TGAATTTCCCT	AACAAGGAAT	ACGACTTATA	CAAATCCCTT	360
TTATCCAGTA	AGATTGATGG	AGGTTGGGAC	TGGGGGAACG	CCGCTAGGCA	TTATTGGGTC	420
AAAGGCGGGC	AATGGAACAA	GCTTGAAGTG	GATATGAAAG	ACGCTGTAGG	GACTTATAAA	480
CTATCAGGGC	TTAGAACTT	TACTGGTGGG	GATTTAGACG	TGAATATGCA	AAAAGCCACT	540
TTGCGTTTGG	GCCAATTCAA	TGGCAATTCT	TTCACAAGCT	ATAAGGATAG	CGCTGATCGC	600
ACCACGAGAG	TGAATTTCAA	CGCTAAAAAT	ATTTCAATTG	ATAATTTTGT	AGAAATCAAT	660
AATCGTGTGG	GTTCCTGGAGC	CGGGAGAAAA	GCCAGCTCTA	CGGTTTTGAC	TTTGCAAGCT	720
TCAGAAGGGA	TCCTAGCAG	TAAAAATGCG	GAAATTTCTC	TTTATGATGG	CGCCACGCTC	780
AATTTGGCTT	CAAACAGCGT	TAAATTAAAT	GGTAATGTGT	GGATGGGCCG	TTTGCAATAC	840
GTGGGAGCGT	ATTTAGCCCC	TTCATACAGC	ACGATCAACA	CTTCAAAAGT	TCAAGGGGAA	900
GTGGATTTTA	ACCATCTCAC	TGTGGGGGAT	CAAAACGCCG	CTCAAGCGGG	CATTATCGCT	960
AGCAATAAGA	CTCATATTGG	CACACTGGAT	TTGTGGCAAA	GCGCCGGGTT	AAATATCATT	1020
GCCCCTCCAG	AAGGTGGCTA	CAAGGATAAA	CCTAATAGTA	CCACTTCTCA	AAGTGGCACT	1080
AAAAACGACA	AGAAAGAGAT	CAGTCAAAAT	AACAATAGCA	ACACAGAGGT	CATTAAACCA	1140
CCCAATAACA	CGCAAAAAAC	AGAAACTGAA	CCCACCAAGT	CATTGATGGG	CCTTTTGCTG	1200
AAGGCAAAGA	CTCGGTTGTC	A				1221

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

780

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066

GTAATAAATA	CAACTAGTAT	GCTAAAAAAA	ATATTTTAA	CCAACAGCTT	AGGGATTTTA	60
TGCTCTAGGA	TTTTTGGCTT	TTTACGGGAT	TTAATGATGG	CCAATATCCT	AGGGGCTGGG	120
GTGTATAGCG	ATATTTTCTT	TGTGGCTTTC	AAATGCGCTA	ATCTATTCAG	GCGTATTTT	180
GCGGAGGGCT	CTTTTTCTCA	AAGCTTTTTA	CCGAGCTTCA	TACGGAGTTC	CATTAAGGGG	240
GTTTTTGC GA	GTTTGGTGGG	GCTTATTTTT	TGTGGCGTTT	TATTCATGTG	GTGCTTATTA	300
GTAGCGCTCA	ATCCCTTATG	GCTAACCAAA	CTCCTAGCTT	ACGGCTTTGA	TGAAGAAACG	360
CTCAAACAT	GCACCCCTAT	TGTAGCGATC	AAATTTTGGT	ATCTTTTATT	GGTGTTTATC	420
ACCACTTTTT	TAGGCGCGCT	TTTACAATAC	AAACACAGCT	TTTTTGCCAG	CGCTTATAGC	480
GCAAGCTTAC	TCAATTTATG	CATGATTTTA	GCCCTTTTGA	TTTCTAAAGA	AAAAACGCAT	540
TTAGAAGCGT	TGATTATT	GAGCTATGGC	GTGCTTTTAG	GGGGCGTGGC	TCAAATCTTA	600
TTACACTTTT	ATCCTTTAGT	AAAATTAGGC	TTATGGGATT	TATTATTTAA	AGGGTTGTTG	660
GGTTTTTAAGA	CTAAAAATAC	AAACAAAAAA	GAATATCGTT	TGAATAGGGC	TAAAAAGGAT	720
CTAAAAGCGT	TTTTCAAGCA	ATTCTTCCCC	AGCGTCTTAG	GCAATTCTAG	CGCTCAGATC	780
GCTTCTTTTT	TAGACACCAC	AATCGCTTCT	TTTCTGGCGA	GCGGGAGCGT	GTCTTATTG	840
TATTACGCCA	ATAGAGTCTT	CCAGCTCCCT	TTAGCCTTAT	TCGCTATCGC	TATCTCCACA	900
GCTCTTTTCC	CTAGCATTCG	GATCGCGCTT	AAAAACAACC	AGCAGGATTT	AATCTTACAA	960
CGCTTGCAAA	AGGCGTGGTT	TTTTTTGGTG	GGGGTTTTGC	TTCTTTGCAG	CATTGGGGGG	1020
ATAATGTATA	GCAAAGAAAT	CACCGAACTT	TTATTTGAAA	GGGGGCAATT	TAGCCCTAAA	1080
GACACCCATA	CTACTTCGCA	AGTCTTTTCG	CTCTATCTTT	TAGGCTTGCT	CCCTTTTGGG	1140
CTAACCAAA	TCTTTTCTTT	ATGGCTTTAT	GCGAAATTAG	AGCAAAAAAA	AGCGGCTAAA	1200
ATCTCTTTAA	TTTCGCTTTT	TTTAGGTTTA	GCGGCTTCTT	TGAGTTTAAT	GCCTTTGTTA	1260
GGGGTTTTGG	GTTTGGCT					1278

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067

TTTCGCTTAC	CAAGTCCCCT	TACCTCAATT	TTAATGCGCC	TAGATTACGC	CCTATTCAAC	60
CAGCATTTAG	CAATAGCAG	AGAAAAAGCT	AAAGCGTTGG	TTTTAAAAAA	ACAGGTTTTA	120
GTCATAAAAA	TGGTGGTTTC	TAAACCCCTC	TTTATCGTTA	AAGAGGGCGA	TCAAATTGAA	180
CTCATCGCTC	CCAATCTATT	CGTTAGCAGG	GCTGGGGAAA	AATTAGGGGC	TTTTTTAGAA	240
GATCATTTTA	TAGATTTTAA	AGAAAAGGTT	GTTTTAGATG	TGGGAGCGAG	TAAGGGAGGC	300
TTAGTCAAG	TGGCTCTTTT	AAAAGGGGCT	AAAAGGTGTC	TTTGCGTGGA	TGTGGGGAAA	360
ATTGAATTAG	TTGAAAGTTT	GAAAAACGAC	CAACGCATAG	AATGTTACGA	AGAATGCGAT	420
ATTAGAGGT	TTAAAACGCC	AGAAAAAATT	GATTTAGCAC	TTTGTGATGT	GAGCTTTTAT	480
TCTTTATATT	GTATTTTAGA	AGCGATTTTG	CCTTTAAGCG	GTGAATTTT	AACGCTTTTC	540
CCGCAAT	TTGAAGTGGG	CAGAACAATA	AAACGCAATA	AAAAGGGGGT	GGTGATGGAT	600

SUBSTITUTE SHEET (RULE 26)

781

AAAGAAGCCA	TTTTGAACGC	TTTAGAAAAC	TTTAAAAACC	ATTTAAAAAC	AAAGGATTTT	660
CAAATCTTAA	CGATCCAAGA	AAGCTTAGTG	AAAGGGAAAA	ACGGGAATGT	TGAATTTTTT	720
ATCCATTTC	AGCGAGCC					738

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068

AGACATGTGC	AACCGATGAA	ATCTAAAAAA	CTTTATTTAG	CTTTAATCAT	AGGGGTTTTA	60
TTAGCGTTTT	TAACCCATATC	TTCATGGCTA	GGTAATAGCG	GTTTAGTGGG	GCGTTTTGGG	120
GTGTGTTTTG	CCGCAATCAA	TAAAAAATAT	TTTGGGTATC	TTTCATTGAT	TAATTTACCC	180
TATTTGGCGT	GCGTTTTTAT	CTTTTATAC	AGGGCTAAAA	ACCCTTTTAC	AGAAATCGTT	240
TTAGAAAAAA	CTTTAGGSCA	TCTATTAGGC	ATTTTATCTT	TACTCTTTTT	GCAATCTAGC	300
CTGTTGAATC	AAGGGGAAAT	CGGCAACAGC	GCGCGTTTGT	TTTTACACCC	TTTTATAGGG	360
GACTTTGGGC	TTTATGTGCT	GATAATGCCT	ATGGTAGTGA	TCTCTTATTT	AATTTTATTC	420
AAACTGCCCC	CTAAAAGCGT	TTTTTACCCT	TATATGAACA	AAACACAAAG	CCTTTTAAAA	480
GAGATTTACA	AACAATGCTT	GCAGGCCTTT	AGCCCTAATT	TTAGCCTGAA	AAAAGAGGGT	540
TTTGAAAAAC	CCCCATCAGA	TTCTCAAAAA	AAAGAAACCA	ACAACGACAA	AGAAAAAGAA	600
AACCTCAAAG	AAAACCCCTAT	TGATGAAAAC	CACAACACCC	CTAACGAAGA	ATCGTTTTTA	660
GCGATCCCTA	CCCCCTATAA	CACGACCTTA	AATAATTTCAG	AGCCGCAAGA	AGGCTTAGTC	720
CAAAATTTCC	CACACCCCCC	TACCCATTAC	ACCATTTACC	CTAAAAGAAA	CCGATTTGAT	780
GATTTGACTA	ACCCCACTTT	AAAAGAACCT	AAGCAAGAAA	CCAAAGAAAG	AGAACCCACG	840
CTAAAAAAG	AAACGCCAC	CACACTCAAA	CCTATCATGC	CCATATCCGC	ATCCAACACA	900
GAAAATCATG	ACAAACAGA	AAACCACAAA	ACCCCTAACC	ACCCCATAAA	AGAAGATGAT	960
TTACAAGAAA	GCCCACAGA	AAACCACAAA	AAAGAAAATA	TAGAAGAAAA	TATAGAAGAA	1020
AAAGAAACGC	AAAACGCTCC	AAGCTTTAGC	CCACTAACCC	TCACCAGCGC	TAAAAAACCC	1080
GTTATGGTTA	AAGAATTGAG	CGAAAATAAA	GAGATATTAG	ACGGGTGGA	TTATGGCGAA	1140
GTGCAAAAAC	CCAAAGATTA	TGAGCTTCCC	ACAACGCAAT	TATTGAATGC	GGTTTGCTTG	1200
AAAGAAACTT	CTTTAGACGA	AAACGAGATT	GACCAAAAAA	TCCAGGATTT	ATTGAGCAAG	1260
CTGCGCACCT	TTAAAATTGA	TGGCGATATT	ATACGCACTT	ATTCAGGCC	TATTGTAACC	1320
ACCTTTGAAT	TCCGCCACGC	CCCTAGCGTT	AAGGTGAGCC	GTATTTTAGG	CTTGAGCGAT	1380
GATTTAGCGA	TGACTTTATG	CGCTGAATCC	ATCCGCATT	AAGCCCTAT	CAAAGGTAAA	1440
GATGTCGTTG	GTATTGAAAT	CCCTAACAGC	CAAAGCCAAA	TTATTTATTT	AAGAGAAATT	1500
TTAGAAAGCG	AATTGTTTCA	AAAATCCAGC	TCGCTCTTAA	CCCTAGCTTT	AGGCAAAGAC	1560
ATTGTGGGTA	ACCCTTTTAT	CACGGATTTA	AAAAAGCTCC	CCCACTTGCT	CATCGCCGGC	1620
ACGACAGGGA	GCGGTAAGAG	CGTGCGCGTG	AATGCGATGA	TTTTATCCTT	ACTTTATAAA	1680
AACCCCTCTG	ATCAACTCAA	ATTAGTGATG	ATCGATCCCA	AAATGGTGGA	ATTTAGCATT	1740
TATGCCGACA	TCCCTCATTT	ACTCAGCCCC	ATTATCACTG	ACCCTAAAAA	AGCTATCGGG	1800
GCTTTGCAAA	GCGTGGCTAA	AGAAATGGAG	CGCCGATACT	CTTTAATGAG	CGAATACAAG	1860
GTTAAACCA	TTGATTCTTA	TAATGAACAA	GCCCCAAGTA	ACGGCGTTGA	AGCGTTCCCC	1920
TATTTGATTG	TGGTGATTGA	TGAATTAGCG	GATTTGATGA	TGACAGGGGG	CAAAGAAGCG	1980
GAGTTTCCTA	TCGCTAGAAAT	CGCTCAAAATG	GGGCGAGCGA	GCGGCTTGCA	CCTCATTGTG	2040
GCGACCCAAC	GCCCCAGCGT	GGATGTCGTA	ACCGGCTTGA	TTAAACCAAA	CTTGCCTTCA	2100
AGGGTGAGTT	TAGGGTAGG	CACTAAGATT	GATTCTAAAG	TGATTTTAGA	CACCGATGGG	2160
GCGCAAAGCT	TACTAGGAAG	GGGCGATATG	CTCTTTACCC	CCCCAGGAAC	AAACGGGTGA	2220

SUBSTITUTE SHEET (RULE 26)

782

GTGCGCTTGC	ATGCCCCCTT	TGCCACTGAA	GATGAAATCA	AAAAAATCGT	GGATTTTATT	2280
AAAGCCCAAA	AAGAGGTGGA	ATACGATAAA	GATTTCTTGC	TAGAAGAATC	GCGCATGCCT	2340
TTAGACACCC	CTAAGCTATCA	AGGCGATGAC	ATTCTAGAAA	GGGCTAAAGC	GGTGATTTTA	2400
GAAAAAAGA	TCACTTCTAC	GAGCTTTTTC	CAACGCCAAT	TAAAAATCGG	CTACAACCAA	2460
GCCGCCACCA	TTACTGACGA	ATTAGAAGCT	CAAGGCTTTC	TATCCCCAAG	AAACGCCAAA	2520
GGCAACAGAG	AGATTTTGCA	AAATTTT				2547

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069

AATTACCTAA	AAATTTTCATG	TTCAAGGATA	GCCATGAACC	CCCAGATTCA	ACCCGCCACT	60
AAAAAACCCCT	TAAATCCCT	TTAGCCGCT	AGTTCAGGCA	ATTTAGTGGG	ATGGTATGAT	120
TTTTACGCTT	ATGCGTTCCT	TGCTCCTTAT	TTCCGTAAGG	AATTTACCCA	CACCAATGAC	180
CCTACTCTAG	CGCTCATCTC	AGCTTTTTTA	GTTTTTATGC	TAGGGTTTTT	CATGCGCCCT	240
TTGGGGAGTT	TGTTTTTTGG	TAAATTGGGG	GATAAAAAGG	GGCGTAAAC	TTCCATGGTG	300
TATTCATTAA	TCTTATGGC	GCTAGGCTCT	TTCATGCTCG	CATTGCTCCC	CACTAAAGAA	360
ATCGTAGGGG	AATGGGCGTT	CTTGTTTTTA	TTGTTAGCCA	GGCTTTTACA	GGGCTTTAGC	420
GTGGGAGGAG	AATATGGCGT	GGTCGCCACT	TATCTCTCTG	AATTAGGCCA	GAATGGTAAA	480
AAAGGTTTTT	ATGGCTCTTT	CCAATATGTA	ACTTTAGTGG	GAGGGCAACT	CTTAGCTATT	540
TTTTCGTCT	TTATCGTTGA	AAACGTTTAC	ACGCATGAGC	AAATCAGCGC	GTITGCTTGG	600
CGTTATTTAT	TCGCTTTAGA	GGGTATATTA	GCCCTACTCT	CGCTCTTTTT	GAGAAATATC	660
ATGGAAGAAA	CTATGGATAA	TGAAGCGACT	CCTCAAAAAA	AGACTAATGT	AAATAATACA	720
AAAGAAACCC	ATATCAAAGA	AACCCAAAGA	GGCAGTTTAA	AGGAATTGCT	CAACCATAAA	780
AAAGCCTTAA	TGATAGTCTT	TGGGCTAACT	ATGGGAGGGA	GTITGTGCTT	TTACACTTTT	840
ACGGTGTATT	TAAAAATCTT	TTTAACCAAC	AGCTCATCGT	TTAGCCCTAA	AGAAAGCAGT	900
TTTATCATGC	TTTTAGCGCT	CTCTTATTTC	ATCTTCTTAC	AACCCTTATG	CGGGATGCCT	960
GCGGATAAAA	TCAAACGCAC	CCAAATGCTG	ATGGTTTTTG	CGATCACAGG	GCTTATTGTA	1020
ACGCCTATTG	TCTTTTATGG	TATCAAGCAT	GCCACTAGCG	TGTATGAAGC	CCTATTTTAT	1080
GAAATACTCG	CATTGAGCAG	CATGAGTTTT	TACACTTGCA	TTGCTGGGGT	TATTAAGGCG	1140
GAATTATTCC	CTGAACATGT	GCGAGCGCTT	GGCGTGGGTT	TAGCCTATGC	GATCGCCAAT	1200
GCGCTTTTTG	GAGGGAGCGC	GAGTTATATA	GCGTTAGAGT	TCAAACAGCA	TGGTTTTGAA	1260
GAGGGGTTTG	TGGGCTATGT	CATGTTGAGT	ATTGTTATCT	TTATGGTTAT	GTTTATCATA	1320
TTCCCTAAAA	AAACCTATTT	GGAG				1344

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

783

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070

AAATGGAAAA	ATTGATGCA	ATTGAGTAAC	GCTGATTAG	AACGATTAAA	AAGCATGGCG	60
AACACGCTTC	GCTTTTTGTG	TGCGGACATG	ATAGATAAGG	CTAATAGCGG	GCATCCAGGC	120
GTGTGTTTAG	GGCTAGCTGA	TGTGATGGTG	GTTTTAAGCT	TGCACCTCAA	CCTAAACCCC	180
ACCAACCCTA	AATGGCTCAA	TAGGGACAGG	TTGGTTTTTA	GCGGAGGGCA	TGCGAGCGCG	240
TTAGTGTATA	GTTTGTGCA	TTTGTGGGGC	TTTGATTGA	GTTTAGACGA	TTTAAAGCGT	300
TTCAGGCAAT	TACACTCTAA	AACCCAGGA	CACCCGTAAT	TACACCACAC	CGAAGGCATT	360
GAAATCACCA	CAGCGCCTTT	AGGGCAAGGT	TTTGCTAACG	CTGTAGGCTT	TAGCATGGCG	420
AGCCAATACG	CTCAAACCTT	TTTAGATAAA	GAGGCGATTT	CTCATAAAGT	CTATTGCTTG	480
TGTGGGGATG	GGGATTTGCA	AGAAGGCATT	AGTTATGAGA	GCACTTCTTT	AGCCGGGCAC	540
CTTCGCCTTG	ATAATCTCAT	TGTGATTTAT	GACAGCAACC	AGATCAGCAT	TGAAGGCGCT	600
ATTAATATTA	GTTTTAGCGA	ACAGGTTAAA	ACACGCTTTT	TAGCGCAAAA	TTGGGAAGTG	660
CTAGAATGCG	ATGGGCATGA	CTATCAAGCG	ATTTCATAACG	CTTTAGAAGA	AGCCAAAAAA	720
TCCCATAAAC	CCACGCTTTT	AATCGCTCAT	ACGATCATTG	GTAAGGGGGC	TATTGGCTTA	780
GAGGGGAGTG	AAAAAACGCA	TGGCTCGCCT	TTAAGTAAAG	AAGTGTGAA	ACAATCCAAA	840
GAAACGCTC	AAATCAATCC	TAACGAAAGC	TTTATAATTA	GCCCCAAAAA	CAAAATGCAT	900
TTTGAAGAAG	TGAAAGTTAG	GGGTATTAGT	TTAGAAGCCT	TATGGGAAAA	GTCTTAAAGC	960
CCTAAACAA	AAGAAAAGAT	CCATGCGTTA	AAGAATTTTG	ATTTTAAACG	CATTAATTAC	1020
CCCCGCTTTA	AAAAAGGCGA	ATCTCTAGCC	ACGAGAGTGA	GTAACGGCAT	GATTTTAAAC	1080
GCTATCGCTA	AAGAATGCGA	GGGCTTTTTA	GGAGGGAGTG	CGGATTTAGC	CCCATCCAAT	1140
AACACGCATT	TGAAACACTC	TGCGGATTTC	CTTTAGGGC	AAAACCTGCA	TTTTGGGATC	1200
AGGGAGCATG	CCATGGGGGC	TATCACTAAC	GCTTTAGCGG	CGTATGGCTT	GTTTGTGCCT	1260
TTTTGCGCGA	CCTTTTTTGT	GTTTAGCGAT	TATTTAATGC	CTAGATTTCG	TTTGAGCGCT	1320
TTAATGAAAT	TAAAAGCCCT	TTTATCTTC	ACGCATGACA	GCATTGGGGT	GGGCGAAGAC	1380
GGGGCGACGC	ACCAGCCCAT	AGAGCAATTG	AGCCATTTAC	GAGCCTTGCC	GCATTTCTAT	1440
GCTTTTCAGGC	CTAGCGATGC	TTTTGAAAAT	AAGGCTTGCA	TGCAAGTGGC	ATTAAGTTTG	1500
AACGCCCCCTA	GCGCTCTTAT	TTTATCGCGC	CAGAATTTGT	CCGTGCTTGA	TGAGGTTTCT	1560
AAAGAGCAGG	TTCTAAAAGG	GGCGTATGTT	AAACACCACT	CTAAAGATCC	CATTATCACG	1620
CTTGTTGCGA	CGGGGAGCGA	AGTCTCTTTA	GCTTTAGAGA	GCGCTAAGAT	TTTAGAGCGA	1680
GAAAATATTTC	CCACTCAAGT	AGTGAGCGCG	CCATGCTTTG	ACTTGTGGT	AGAGCAAGAT	1740
GAAAGCTATT	TTAAAGAACT	CTTTAAGGGT	AAAGTCTTAG	TGATTGAAGC	GAGCCGCGCG	1800
ATAGAGTGGT	ATCGTTTTGC	GGATAAAATC	ATTGGCATGG	ATTCTTTTGG	GAGCTCAGCA	1860
AAGGGCGATA	AACTCTTTGA	AAAATTGGC	TTTAGCGTTG	AAAACATTAC	CGCTCAAGCG	1920
AAAAGGTTAC	TCAACGCA					1938

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori***SUBSTITUTE SHEET (RULE 26)**

784

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071

AAGGATTATT	GCATGCAAAA	TGGGTATTAT	GCGGCCACAG	GGGCAATGGC	TACACAATTT	60
AACCGCTTGG	ATTTAACCTC	TAACAATTTA	GCCAACCTAA	ACACCAACGG	CTTTAAAAGA	120
GACGATGCGA	TTACAGGCGA	TTTTTTAAGG	CTTTACCAAG	AATACCGAGA	GCAACTGCCC	180
TTAGAAGATC	AAACCAAAGC	GAGCGCGAAG	TATCTCAACC	GCAACCTCAA	TCGTGTGCCT	240
ATTCTATCAG	AAATCTATAC	GGATAGGAGT	CTTGGCGCGT	TTGAAGGGAC	GAATAACCCC	300
CTAGATTTTG	CCCTAACAAAG	CCCTAACCTC	TATTTTGCGA	TACAGACTAA	TGAGGGCGTC	360
GCTTATACCA	AAGACGGGCA	TTTCAGCGTT	GATAAAGACG	GCTTTTTGGT	AACCCTTAAT	420
GGTTTTAAGG	TGCTTTCACG	CTCCGGTTTG	AACGAAAAAG	GAGGGATCAT	GCTCATGCTT	480
AACGCTGAAA	TTGAAGTGGA	TCAAAATGGT	GGAATCACIT	TTAGGGATAA	TGAAGCCCAA	540
ATTCAAGCGG	GCGCGTTGGC	TTTAGTGAGT	TTTAGCGAAC	CTAAAAATCT	TAAAAAAATA	600
GGGCAAAACC	TTTATACCTA	TCAGGGCGAA	GGCGTTCATC	AAGTCTCTGA	CTCTGGTGCG	660
TTAAGGCAAT	CCATGCTAGA	AAAAAGCAAT	GTCAATGCGG	TGCGTGAGAT	GAGCACTTTG	720
ATTGAAATCA	ACCGCTTTTT	GGACATGTAT	TCTAAAGTGC	TAAAAACCCA	TCAAGATGAC	780
ATGAACGCTG	AAGCGATTAA	CAAACTCGCT	ACAAAAGCT			819

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072

GGAATGATAG	CGCTGAATTT	CAACCTCTTA	GATAAAGAAA	CAAACACGCC	CTTATTTGAA	60
AAAAGCCCCG	TAGATTCAAG	CTTAGAGCTA	TATAAAAATA	GCGAAATTCA	CATGCTCTAT	120
CCTTATTTGT	ATTATTTTGG	CTTGGGTAAT	GGGGTGTTTT	ATCGCTTGCT	TTTAGGCAAT	180
GAAAAATTTAA	AACGCTTGGT	GGTCATTGAG	CCTGAAATAG	AGGTGATTTT	CATTGTGCTG	240
AATCTTTTGG	ATTTTTCAC	TGAGATTTTA	GAAAATCGTT	TGATTTTATT	GCATGCAAGT	300
TTTTGCAATT	ACAACATGAT	TGCTTCATTA	TTTGATATGG	ATAAAAAGTC	TCGTTTATAC	360
GCAAGAATGT	ATGATTTAAA	ACTTTTAAAC	GCTTATATG	AACGATACTC	TCATCAAATG	420
ATAGAAATCA	ACCAGCATTT	CACGCGCGCT	TTAGAGCATG	GCGCTATTAG	CGTAGGCAAT	480
GACGCTAAAG	ACGCACTCAT	AGGCATCAAA	CAGCATGTCT	CTAATTGCCC	TGAAGTCATC	540
AAAAGCCCTA	GTTTAGTGGA	TTTTGTGAAC	GCTTTAAAAA	ACAGAGACAC	CGCTATTATC	600
GTTCACACCG	GGCCTAGTTT	AAATAAGCAA	CTCCCCCTTT	TAAAAAGAAAT	CGCTCCTTAC	660
GCAACGCTTT	TTTGCATAGA	CGCTTCTTTC	CCTATTCTAG	CCAGAGCCGG	TATCAAGCCT	720
GATATTGTGC	TGCTTTTAGA	AAGGGTGGAT	TTAACGGCGA	AATTCTATGA	AGAAACCCCC	780
TTAGATTTTC	AAGAAGGCGT	TATTTTGTCT	CTGACTTCCA	TTGTGCATAA	ACGATTGATT	840
CAAGCGATTTC	AAAAAGGGGT	TAAGCAATTTC	AGTTTCCGCC	CCTTTGGCTA	TACCAACCTT	900
TTTGTATTGC	ACCAGTATGG	TTATGTGGGC	ATAGGCATGA	GCGCAGCGAA	CATGGCGTAT	960
GAATTAGTGG	TGCATCTCTG	TTTCAAAGGG	TGCGTGTTTA	TCGGGCAAGA	TTTGAGCTTT	1020
TCACAAAGCG	GTAACAGCCA	CGCTAGTGGG	GCGATTATATG	GCGATAGAGA	GATCAAGCCT	1080
AAAAAGGATA	AAGACAAGAT	TTTTATAGAA	AAATACGGGG	GTAATGGGAA	AGTAGAAACC	1140

SUBSTITUTE SHEET (RULE 26)

785

ACTTTAGTGT	GGAAACTTTT	CTTAGAATTT	TTTGAAAAAG	ATATTTTAA	CACGCCCTAT	1200
AAATTAGAAG	TCATTAACCC	TACTGAGGGG	GGGGCTAGGA	TTAAAGGGAC	TAAAGAAATG	1260
CCCTTTAAAG	AAGTGTGCGA	AAAAATAGAC	AAATCCAAGC	CAAAGCCTCC	TATCAATCTT	1320
ATTTATCCCA	CCCAATCAGA	ACAGGCTAAA	AATTTAAAGA	TCGCCAAGAA	AAAATGCGAA	1380
GAGATCATCA	AATACGCCAA	TGAGAAAAAA	ACGCAAGTTG	AAGAAGCGTT	TTTAAAGGTG	1440
GCAGAGTTT	TAGAAAAAGT	GGAAAAGCTT	CATGAAAAAA	ACAAATTAGA	AGAGTTGGAT	1500
TTTGAAGAAT	TAGAAAATTT	GAGCGCTGAA	ATTGATAACG	TTAAAGAGCT	TTTGTATGAC	1560
AAACGATTCA	ATTTCGTATT	TATGGATGCG	ATACAATCTT	ACATTTTCCA	CCAGGAATG	1620
CATATCGCTG	AAATCGTGTG	TAAAAAACG	AGTAATGAAG	ACGGATTAAG	GGCTAAGCAA	1680
TTAGAATACA	TTACGCGCA	CAAATACTGG	CTTTTAGTT	TAGCGGGTGG	GATGGATTGC	1740
GTGATAGAAG	CGATCAAAAT	GGCTTTGAAA	GAATGG			1776

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073

GTGCATTTTA	CGTGTATCTT	TCTAACCCCTA	TTAAATGGA	TTTTGCCAGC	CAAAAACAAG	60
CAGGCGTGCA	AAAAGCCACC	AACCAGATCC	ATTCAAGGTC	TGCAAAACAT	CCAGCAAAT	120
ATCCCCCTC	AAGTATTAAC	CCCTCAAATC	CAAGCGGGTA	TACAAGGGGT	GATGCAAGGT	180
TTTGGGGCTT	TGAGCAGCAC	TTTAGAAGCC	CCCTTATTGT	TTTCTAAGCA	AAATGTGGTG	240
ATTGGGGGCT	TTGAGCATT	TTTATCCCCT	TTATATGGGT	GGGGCAAGAT	TCACGATGGT	300
CGCATTGCC	GAATTGAATG	CAAAAAGACG	CCAATGAAGT	GTATCGCT		348

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1131

SUBSTITUTE SHEET (RULE 26)

786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074

CGCATGAATT	TTTTTAAAT	CCTTTTAATG	GAGTTAAGAG	CCATTGTTTC	TCATAAGGGC	60
GTTTTATTGA	TCCTTATAGG	CGCTCCTTTA	ATCTATGGCT	TGTTATACCC	TTTGCCTTAT	120
TTGAAAGACA	TCGTAACGCA	GCAAAAAATC	GCCCTTGTTAG	ATGAAGACAA	TTCCCTTCCTT	180
TCTAGGCAAT	TAGCCTTCAT	GGTGCAAAGC	TCCAACGAGT	TAGAAATCGC	TTTCTTTAGC	240
CCCTCTATGC	TGGAAGCCAA	AAAGCTTTTA	AAAGAAGAAA	AAATTTATGG	GATCTTACAC	300
ATTCCTCTCTC	ATTTTGAGC	CAATATTTAT	AAACAAGTGC	CTGTAACGAT	AGATTTTTAT	360
GCGAACGCCA	ATTACTTTTT	GATTTATGGT	GCGTTAGCGA	ATGCGGTGGT	GGGGAGCATC	420
AACGCCTTAA	ACGATGAAAT	CAGGTTCAAA	CGCAACGCCC	AAATAGAAGA	AGCTGAATTA	480
GGGACAGACG	GGATTAAAGT	TAAGCCTATC	GCTTTGTATA	ACCCTAGTGA	GGGGTATTTG	540
AATTACGCGC	TCTCTAGCGT	GTTTATTTTC	ATCTTACACC	AGGTGATGCT	CATTGCAAGC	600
AGCATGTTTA	CTAGCTCCAG	GCGTTTGGAA	TTGGCCCTTT	TAGACAAGAA	ACAAATCGCT	660
TTAAGGCTGT	GCGCAAGACT	CTTGGTGTTT	ATGGGGGCGT	TTAGCGTTTT	TGTTTTATGG	720
TATTTTGGGG	CGCTGTTTTT	TTTTTATGGG	ATCGAACGGC	ATGGAAGCGC	TTTAATGGTG	780
TTTTTTGAACA	GCTTGATTTT	CATGCTTGCG	GCCTTGAGTT	TGGGGTCGTT	TTTAGGGGCA	840
TGGATCAAAA	ATGAAGCCCA	CACCACTCAA	ATCGTTTTGA	TTTCTTCTTT	GCCCTTGATT	900
TTTATGATGG	GTTTTGTGTG	GCCTTTTGAA	TCCTTGCCCT	CTTATTTGCA	AGTCTTCGTT	960
CAAATAGTGC	CTGCTTATCA	TGGGATCAGT	TTGCTCGGGC	GATTGAATCA	TATGCATGCG	1020
GAATTTATAG	ATGTTTATAT	CCATTTTAC	GCGCTTATTG	CGATTTTTAT	CGTGAGTTTT	1080
ATAGGGTGCG	TGTTCAAAT	CAGCTCTTTA	AAGAAAGCTT	GTGAAAACGC	T	1131

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075

ACCTTAAAAG	GGATTGTTTT	GTTTCAGATTG	ATAAGCGCAT	GGGTTTTACA	AGACAAGTTC	60
TTGTTTGTCT	TGTGTTTTAT	ATTGCCTTTT	TGTTTAGGGG	TTTTAGGCAC	GCAAATCTTT	120
AAACAAGAGA	CCCCAAGACA	GCTCCCTATC	GTGGTGTTGG	ATTTGGATAA	GACCACTACA	180
AGCCATCAAG	TGGCGTTTGA	ATTAGGCGCA	ACGAGTGGCG	TTGAAATCAA	ATACCAAGTG	240
ACTAGCCTTT	CAGAAGCTAA	ACGCTTTT				267

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

787

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076

AGCATGAAAA AAACAACCCT CTTGTATTG GGCTTATTAT TCAATAGCTC TTTAAGCGCT	60
GTTGATGGGA TTTCTCAAAC CGAGCCTTCT TCTTTGAATT TGGCTGAAGA TAGCCTGCCT	120
TTGAACCAT CTAAAGCCCA AAAACTCTCT TTA AAAAAG CATGGAATAG GGTGTTGTCT	180
AATCATGAAG GCTTGCATGC GCAGAATACG CCATTAAGCG AGCGAGTAAA A	231

(2) INFORMATION FOR SEQ ID NO:1077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077

GTAAGGAGAC AAACATGAA AAAGGTTATT GTGGCTTTAG GCGTTTTGGC GTTCGCAAAT	60
GTTTAAATGG CAACCGATGT TAAGGCTCTT GTAAAAGGTT GTGCCGCTTG CCATGGGGTT	120
AAGTTTGAAA AGAAAGCTTT AGGTAAAAGC AAAATCGTTA ACATGATGAG CGAAAAAGAG	180
ATTGAAGAGG ATCTTATGGC TTTTAAAAGC GGTGCCAACA AGAATCCTGT CATGACCGCG	240
CAAGCTAAAA AATTAAGCGA TGAAGACATC AAAGCTTTAG CCATATACAT CCCCCTCTC	300
AAA	303

(2) INFORMATION FOR SEQ ID NO:1078:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

788

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078

AGACCTATGC TACATAAAAA ATATCGTCCT AATGTTGCGG CCATTATCAT GTCGCCAGAC	60
TACCCTAACA CATGCGAAGT TTTTATCGCT GAGCGCATAG ACATTGAAGG GCGGTGGCAG	120
TTCCCCAAG GAGGCATTGA TGAGGGAGAG ACCCCTTTAG AAGCACTCTA TAGAGAATTA	180
CTAGAAGAAA TTGGCACGAA TGAAATAGAG ATTTTGCGCG AATACCCTAG ATGGATCGCC	240
TATGATTTC CAAGCAACAT GGAGCATAAA TTCTATTTCG TTGACGGGCA AAAGCAGCGT	300
TATTTTTTAG TGCGCCTAAA GCATGTTAAC AACATTGATT TGAACAAACA CACGCCAGAA	360
TTTATATCCT ATCAATTCAT CCAGCTTAAG GATTTGCTTA AAAAAATCGT TCCCTTCAAA	420
CGCCAAGTGT ACCGCCAAGT CATCGCTTAT TTTAGAAAAG AGGGGTATT GGGGTGT	477

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079

TGCATGAATC TTGCTTTTT GTGGGCCGCT CTAGGAGGGG CTATAGGGAG CTCGTTAAGG	60
TATTTTGTGG GCAAAATGAT GCCCAGTAAA TTTTAAATGT TTGAAAGTTT CCCTTTAGGG	120
ACTTTTAGCG TGAATCTCAT AGGGTGTTTT ATCATCGGCT TTATGGGGCA TTTGGCCGCT	180
AAAAAAGTTT TTGGTGATGA TTTTGGGATT TTCTTTGTAA CCGGAGTTT AGGGGGTTTT	240
ACGACCTTTT CTTCTTATGG GTTAGACACT TTAAAACTCT TGCAAAAATC CCAATACCTT	300
GAAGCCATTT CTTATGTCTT AGGCACTAAC CTTTATAGGGC TTATTGGGGT AGCTATCGGT	360
TGGTTTTTGG CTAAGAATTT TGTAGGCGTT AAT	393

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

SUBSTITUTE SHEET (RULE 26)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080

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TATTTATCAA TCGTGGTGGA AGATCAGAAA GGCATTTTCC CTATCGCAGC GTCAAAAAGA      60
AAAAGCCAAA GCTCTGTGAT CATTGAAGAC GTGTGCTTCA GCAAAGAGGA TTTTGTAGAA      120
GGGGCAAAAG CGATTGAGGG GCTTTTAAAA AACATGGCT TTAAGGATAA TGGCATTATT      180
TTTGGGCATG CGTTAAGCGG GAATTTGCAC TTTGTCGTTA CGCCGATTCT AGAAAAATGAA      240
GCTGAAAGAA AAGCGTTTGA AAATTTAGTT TCTGAGATGT TTTTAATGGT GAGCAAAAGC      300
TCTGGCTCTA TTAAAGCCGA ACATGGCACA GGCAGGATGG TAGCCCTTTT TGTGGAAATG      360
GAGTGGGGAG AAAAAGCTTA TAAGATCCAC AAACAAATCA AGGAATTGTT TGATCCTAAT      420
GGCCTTTTAA ACCCTGATGT GATCATCACA AACGATAAAG AAATCCACAC TAAAAATTTA      480
AAGAGCATTT ACCCTATTGA AGAGCATTG GACATGTGCA TGGAAATGTGG GTTTTGTGAA      540
AGGATCTGCC CCAGTAAAGA TTTATCCTTA ACGCCACGAC AACGCATCGT CATCCACAGA      600
GAGGTAGAGC GTTTGAAAGA AAGGGTAAGT CATGGTCAAT ATGAAGATCA GGTTTTACTA      660
GATGAGCTTT TAAAGAGTC TGAATACTTA GCGCATGCCA CTTGCGCGGT GTGCCATATG      720
TGTTCACCTT TATGCCCTTT AGGGATTGAT ACCGGGAGTA TCGCTTTAAA TCATTATCAA      780
AAAAACCTTA AAGGCCAAAA GATCTGCTTC AAAGATTCT      819

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(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081

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CGATTTTAC AAAAGAGTGC GCAAATTTGG GGAATTAAAA TGCTAGTAGA AATAGAGAAT      60
TTGACTAAAA CTTATGGGAG TTAAAAAGCG CTAGACAATA TCAGTTTGAA ACTACCCAAA      120
CAGCAATTTA TAGGGCTTTT AGGGCCTAAT GGGGCGGGTA AAACCACTCT GTTAAAAATT      180
TTAGCCGGAT TGAATTTGAA CTATCAAGGG GAAGTGAAAA TTTTAAACCA AAAGATTGGT      240
ATAGAGACTA AAAAAGCGT GCGCTTTTTA AGCGATGCGG ATTTTITAGA TCCTAAATTA      300
ACGCCTTTAA AAGCGATCGC TTTTATAAG GATTTTITTA GCGATTTTGA TGAATCAAAA      360
GCCCTAAATT TGTAAAAACG CTTCAGCGTG CCTTTAAAAA GAGAGTTCAA AGCCCTTTCA      420
AAAGGCATGA GGGAAAAATT GCAGCTGATT TTAACCTAT CACGAAACGC TTCTTTGTAT      480
CTTTTGTATG AGCCGGTGGC TGGGATGAC CCTATTGCAA GAGAAGAGAT TTTTGAGTTA      540
ATCGCTAAGG AGTTTAGCCA AAACGCAAGC TTGCTAGTCT CTACGCATTT GGTGGTGGAT      600
GTGGAAAAAGT ATTTAGACAG CGCGATTTT TTAAGAAGAG CTAAAGTGGT GGCTTTTGGG      660
GATGTGGGGG AATTAAAAAA AGGGTATAGC AGTTTGGAGG CAGCGTATAA AGAAAGGTTG      720
AAA

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(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid

790

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082

AAATCGTGGT	TTTTCTATGC	CCCTTTTAT	GGTTTGTGGT	GTTTAAAAAC	CCCTATCATA	60
GGGCATGGCA	TGAAGAAAA	AGCAAAAGTC	TTTTGGTGT	GTTTAAAAAT	GATTCGTTGG	120
TTGTATTTGG	CGGTCTTTT	TTTGTGAGC	GTATCAGACG	CTAAAGAAAT	CGCTATGCAA	180
CGATTTGACA	AACAAAACCA	TAAGATTTT	GAAATCCTTG	CGGATAAAGT	GAGCGCCAAA	240
GACAAATGTA	TACCGCCTC	AGGGAATGCG	ATCCTATTGA	ATTATGACGT	GTATATTCTA	300
GCGGATAAGG	TCGCTTATGA	CACCAAGACT	AAAGAAGCGT	TATTAGAAGG	CAATATTAAG	360
GTTTATAGGG	GCGAGGGCTT	GCTCGTTAAA	ACCGATTATG	TGAAATTGAG	TTTGAACGAA	420
AAATATGAGA	TCATTTTCCC	CTTTTATGTC	CAAGACAGCG	TGAGCGGGAT	TTGGGTGAGC	480
GCGGATATTG	CTAGCGGGAA	GGATCAAAAA	TATAAGATTA	AAAACATGAG	CGCTTCAGGG	540
TGCAGCATTG	ACAACCCCAT	TTGGCATGTC	AATGCGACTT	CAGGCTCATT	TAACATGCAA	600
AAATCGCATT	TGTCAATGTG	GAATCCTAAG	ATTTATGTCG	GCGATATTCC	TGTATTGTAT	660
TTGCCCTATA	TTTTCATGTC	CACGAGCAAT	AAAAGAACTA	CCGGGTTTTT	ATACCCCTGAG	720
TTTGGCACIT	CCCACCTTAGA	CGGCTTTATT	TATTTGCAAC	CCTTTTATTT	AGCCCCCAAA	780
AACTCATGGG	ATATGACCTT	TACCCACAAA	ATCCGTTACA	AAAGGGGTTT	TGGCTTGAAT	840
TTTGAAGCGC	GCTACATCAA	CCCT				864

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083

ATCGTTAGAA	AGAAGTTAAT	GTTAGAGATG	AGTTTGCAAG	CATTAAATAC	ACAAGATTCT	60
TCTGTGATGG	CTCAATCCTT	GCTTGTCAT	GCCTTTTITG	CCGCCTTGCT	CGCCCTAGCC	120
TTTATGATCA	ATCTTTACAC	CCTTTTAA	GAAAAGAATT	TCATCCAATT	GAACCGGAAA	180
ATCTATCTTG	TCATGCCAGC	GATTATATT	CTTTTAAGCA	TCGCTCTTTT	GAGTGGGGTT	240
TTTATTTGGG	CGATGCAACA	ATTTGAATTT	TCTTTTAGCG	CTGTTGTCAT	GCTTTTGGGG	300
TTGTGTGTTGA	TGCTCATTGC	AGAAATCAAA	CGCCATAAAA	GCGTGAAATT	CGCTATCACT	360
AAAAAAGAAA	GGATGAAAGC	CTATATCAAA	AAAGCTAAAA	TCCTGTATTT	TTAGAAAACG	420

SUBSTITUTE SHEET (RULE 26)

791

ATTCTTATCA TCGTGTTAAT GGGCATT

447

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084

CCAGAAGGAG	GGAATGAACT	CAATGTGTTT	GAGCCGGTTA	TCGCTTACAA	GCTTTTCCAT	60
TCCTTTGTGA	TTTTAGGGTG	CGCGATTGAA	ACTTTAACGA	CTAAATGCGT	GGAAGGCATC	120
ACGGCTAATG	AAAAGATTTG	CCACGATTAT	GTTTTAAACA	GCATTGGCAT	TGTTACCGCG	180
CTCAACCCTC	ATATCGGCTA	TGAAAAATCC	GCTATGATCG	CCAAAGAAGC	CTTAAAAAGC	240
GATCGCTCTA	TCTATGATAT	CGCTTTAGAA	AAGAAAATCT	TAACCAAAGA	GCAACTGGAC	300
GATATTTTCA	AGCCAGAAAA	CATGCTAAGC	CCTCAGCCTT	TCAAAAAGCA	TAAAGAC	357

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085

AAAAGGCTTA	TGTTTTGT	TCTATCCATT	TTTAAAAAA	GCTTTAATGA	TTTTTTAAGC	60
GCTAGAAATG	CTTTAATCAA	TCTTGGCCCT	ATCCTTTTGA	GTITGGCGTT	TTTGGAGCT	120
ATCTTTTATT	ACAATGGCGG	GAGTATTGTG	AATTATTGCC	AAACTTTATT	ACCGCAATCT	180
TTGAATGATT	ACGCTCATTC	TCAAGGCTTT	TTTGCCGGTG	TGTTCCGATG	GGTTTTTAAA	240
GCGTTAGTGT	ATTTTCTTAT	TTTTTGGATC	GTAATCTTTT	TGAGTTTAGT	CATCAATATT	300
TTTGCGTCTA	TTTTTTACAC	CCCTTTAGTG	GTCTCTTATT	TGCACCAAAA	ATATTATCCC	360
CATGTCGTTT	TAGAAGAAAT	TGGCTCTATC	CTTTTTTCTA	TTAAATATTT	TTAAAAATCG	420
CTCACTTTTA	TGCTTTTATT	CTTAGCGGTT	TTAACGCCCC	TTTATTTTCAT	TCCCTTTATA	480

SUBSTITUTE SHEET (RULE 26)

792

GGGGTCTTTG	GGGTCTTTTT	TTCTATAGTC	CCGCATTTC	TCTTTTCAA	AAACACCATG	540
AGTTTGGATA	TAGCCAGCAT	GATTTTCAAC	CATCAAAGCT	ATCAAAATTT	ACTCAAACAG	600
CACCCATTGA	AGCATTATCG	TTTTTCGTTT	TTTIGCTATC	TTTTTTCCTT	GATTCCTTTT	660
TTTAATTTTT	TTGCCACCTT	GTTGCAAACC	CTAATGTAA	CGCAC		705

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086

GAATGTAAAG	GAATGGAATT	TATGAAAAAG	TTTGTAGCTT	TAGGGCTTCT	ATCCGCGGTT	60
TTAAGCTCTT	CGTTGTTAGC	CGAAGGTGAT	GGTGTTTATA	TAGGGACTAA	TTATCAGCTT	120
GGACAAGCCC	GTTTGAATAG	CAATATTTAT	AATACAGGGG	ATTGCACAGG	GAGTGTGTGA	180
GGTTGCCCCC	CAGGTCTTAC	CGCTAATAAG	CATAATCCAG	GAGGCACCAA	TATCAATTGG	240
CACTCCAAAT	ACGCTAATGG	GGCTTTGAAT	GGTTTGGGT	TGAATGTGGG	TTATAAGAAA	300
TTCTTCCAAT	TCAAGTCGCT	AGATATGACA	AGCAAGTGGT	TTGGTTTTAG	AGTGTATGGG	360
CTTTTGTATT	ACGGGCATGC	CGATTTAGGT	AAACAAGTTT	ATGCACCTAA	TAAATCCAG	420
TTGGATATGG	TCTCTGGGG	TGTGGGGAGC	GATTGTGTTAG	CTGATATTAT	TGATAAAGAC	480
AACGCTTCTT	TTGGTATTTT	TGGTGGGGTC	GCTATCGGGC	GTAACACTTG	GAAAAGCTCT	540
GCAGCAAAC	ATTGGAAGA	GCAAATCATT	GAAGCCAAAG	GTCTGATGT	TTGTACCCCT	600
ACTTATTGTA	ACCCTAATGC	CCCTTATAGC	ACCAACACTT	CAACCGTCGC	TTTTCAAGTG	660
TGGTTGAATT	TTGGGGTGAG	AGCCAATATC	TACAAGCATA	ATGGCGTGGA	ATTTGGCGTG	720
AGAGTGCCGC	TACTCATCAA	TAAATTTTTG	AGCGCGGGTC	CTAACGCTAC	TAACCTTTAT	780
TACCATTGA	AACGGGATTA	TTCGCTTTAT	TTGGGGTATA	ACTACACTTT	T	831

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2028

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087

GCTTTTGAAG	AATTAGAGCC	TTTGAGTTTT	TCCTTCAATT	CGCCTAAAGG	GGCGTGCAGAA	60
AGTTGTTTTG	GTTTAGGGAC	AAAATTTAGC	TTAGATATTA	GTAAGATTTT	AGATCCTAAC	120
ACGCCTTTAA	ATCAAGGAGC	GATTAAAGTG	ATTTTTGGGT	ATAACCGCAG	TTATTACGCT	180
CAAATGTTTG	AAGGCTTTTG	CACTTATAAT	GGCATTGACA	GCGCGCTTTG	TTTCAACGAA	240
TTGAACAAAG	AGCAGCAAGA	CGCTCTTTTG	TATGGGAATG	GCACTGAAAT	CAGCTTTTCAT	300
TTTAAAAACA	GCCCCCTGAA	ACGCCCTTGG	AAAGGCATTA	TCCAAATCGC	TTATGACATG	360
TTTAAAGAGC	AAAAGGATTT	GAGCGATTAC	ATGAGCGAAA	AAACCTGTTC	TTCTGTGTAAT	420
GGGCATCGCT	TGAAAGCCTC	AAGTTTGAGC	GTCCAAGTCG	CTGGCTTGAA	AATGGCGGAT	480
TTTTTAACTA	AGCCCATTTGA	AGAAGTCTAT	CATTTTTTTA	ATGATCCAC	GCATTTTAAAC	540
TATCTTAACG	AGCAAGAAAA	AAAGATCGCT	GAACCCATTT	TAAAAGAGAT	TTTAGAAAGG	600
GTGTTTTTTT	TATACGATGT	GGGGCTAGGG	TATTTGACTT	TGGGGAGGGA	TGCGCGAACC	660
ATTAGCGGAG	GGGAGAGCCA	AAGGATACGA	ATCGCCAGTC	AAATCGGGAG	CGGTTTGACA	720
GGGGTTTTGT	ATGTTTTTAGA	CGAGCCTAGC	ATTGGCTTGC	ATGAAAAAGA	CACGCTCAAA	780
CTCATCAACA	CCCTTAGGAA	TTTACAAAAA	AAGGGGAACA	CGCTCATTGT	CGTAGAGCAT	840
GATAAAGAGA	CGATTAAGCA	TGCGGATTTT	GTTGTGGATA	TGCGGCCAAA	GGCTGGAAGG	900
CATGGGGGTG	AAGTGGTTTT	TAGCGGGAGC	GTAAGAAGATT	TATTGCAAAA	TAACCATTTCT	960
ACCGCCTTGT	ATCTCAACGG	CACTAAAAAG	ATTGAGCGCC	CCAAATTTGA	ACCCCTTAAA	1020
GAAAAGCATT	TTTTAGAAAT	TAAAAATGTC	AATATCAATA	ACATTAAGAA	TTTGAGCGTT	1080
CAAAATCCCT	TAAAACAATT	GGTGTGCATT	ACGGGGGTGA	GCGGGAGCGG	TAAAAGCTCG	1140
CTGATTTTAC	AAACCCTTTT	ACCCACCGCT	CAAACCCTTT	TAAACCATGC	TAAAAAAAAT	1200
CAAAGCTTGA	ATGGGGTGGA	GATTGTAGGG	TTGGAGTATT	TGGATAAAGT	GATTTATTTA	1260
GATCAAGCCC	CCATAGGCAA	AACCCACGCA	AGCAACCCCG	CCACTTACAC	GGGAGTGATG	1320
GATGAAATCA	GGATTTTATT	TGCCGAGCAA	AAAGAAGCTA	AAATTTTAGG	CTATAGCAGC	1380
AGCCGTTTCA	GCTTTAATGT	TAAAGGAGGG	CGGTGTGAGA	AATGCCAAGG	CGATGGGGAT	1440
ATTAAATAG	AAATGCACTT	TTTGCTGAT	GTGTTAGTCC	AATGCGATAG	CTGTAAGGGC	1500
GCTAAATACA	ACCCCAAAC	TTTAGAAATC	AAGGTGAAAG	GCAAATCCAT	TGCTGATGTG	1560
TTGAACATGA	GCGTGGAAGA	AGCTTATGAA	TTTTTTTGCTA	AATTCCTTAA	AATCGCTGTG	1620
AAGTTAAAAA	CGCTTTATAGA	TGTGGGCTTA	GGCTATATCA	CTTTAGGGCA	AAACGCTACG	1680
ACTTTAAGTG	GGGGGGAGGC	TCAAAGGATC	AAATTGGCTA	AAGAATTGAG	TAAAAAAGAC	1740
ACAGGCAAAA	CCCTTTATAT	TTTAGATGAG	CCTACCACCG	GTTTGCATTT	TGAAGATGTG	1800
AATCACCTTT	TACAAGTCTT	GCATTCTTTG	GTGGCGTTAG	GCAATTCAT	GCTAGTGATT	1860
GAGCATAATT	TAGACATCAT	CAAAAACGCT	GACTACATTA	TAGACATGGG	GCCTGATGGG	1920
GGGGATAAGG	GCGGGAAGT	CATTGCGAGC	GGCACGCCTT	TAGAAGTGGC	GCAAAATTGC	1980
GAAAAAACCC	AAAGCTATAC	GGGAAAAATT	TTAGCTTTGG	AATTGAAA		2028

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...828
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088

GCGCGTTTTG	TTAAAAACAC	AGCGGATTAT	TTTTCCCTTA	TGAAAAACGT	GTTTACCGC	60
TCCATTACCA	TGACGCTTTT	ACTCTTGCTT	ATCTATCCTT	TCAAACCTTA	CCGCTTGAAG	120
AGTTACAAAC	AAGGCGGTTT	TAAAAAGCTC	GCCTTTAGGG	TCGTTGTGGG	GGGCTTAGCC	180

SUBSTITUTE SHEET (RULE 26)

794

ATGCTGGCGT	TTTTTTATAA	TATTGAAAAA	ATTTCGCTCG	CCACAGCGAA	CGCTTTCTCA	240
CAATGCCGCG	CTATTTATAC	GGTGCTCCTT	TCCCTTTTGC	TTTTGAAAGA	AAAGCTCAAA	300
AGAAGCGCGT	TAATTTCCGC	ATGCATCGGG	CTAGTGGGGG	TGGTGTGAT	TTCAGATCCT	360
AGCGTGGA	ATGTAGGACT	AGTTGAAATC	ATTATGGGCA	TATTGAGCGG	GATCTTTGTG	420
TCTTTAGCGT	ATATCACTTT	AAGGGATTG	AGGGAATATT	ACGACAAGCA	GGCCGTGATT	480
TTAGCGTTTC	CCTTTGGCAT	GAGTCTTCTT	GGATTAGCGG	GCATGTTTAT	TGATATTCCT	540
TTTTTATCCA	CAGGCGTTCA	TATCCCTAGA	AAAGAGGATA	TTTTATGGAT	TTCTTTAATA	600
GGGATTAGCG	GGACTTTAGG	GCAGTATTTT	TTAACCTATG	CTTACATGAA	CGCTCCTGCT	660
GGGATCATCG	CCCCCATTTGA	ATACACCCGC	ATTGTTTGGG	GGCTATTGTT	TGGGCTGTAT	720
TTAGGCGATA	CATTTTTTGA	TCTTAAAGC	TCTTTAGGGG	TGGCTTTGAT	CTTATGTTCA	780
GGCTTGCTCA	TTGCCCTTGC	CGCTCTTTTA	AAAGAATTAA	AAAAAATT		828

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089

GTCATGCAAC	TAAGCCCCTT	ACAAAGCGCG	CTGTTATATT	TCCGTTACTT	TATTTATCCG	60
GAAAAA	CAAGGAGCTT	TGATTAAAGC	GATTTAATTT	TTATTGTCAT	GTTTTTTTTA	120
GTCCTAGCTT	TGGGGCTGTT	GATGAGCGAA	GAAATTTCTA	TCAGCTACAA	TGAAGCGAAA	180
GACTTTTTTT	ATAGCGATGC	GTGGTTTGTC	AAAATCGCTC	AAAAAAGCGT	AGCCATTTTA	240
GGCCAAAACG	ATTTGGCTTT	AAGATTGCCT	TTTTTGATCG	CTCACGTCAT	CAACATGTTT	300
TTATTCTACC	TCATAGGGCG	AAAGATTTTA	AAAAAGCCTA	AAGACGCTCT	TTATGTGTTA	360
TTGACTTACG	CTTTATTGCC	TGGGGTGAAT	CTCTTTGCGA	TTTTACTGGC	TAAAAGCGTG	420
CTGGTGTTAA	GCCTTGGGCT	TTTGATTAGC	TATTTGTATA	TTAAAACCCA	AAAAATCCCT	480
TATTTAACCC	TTAGCGCTTG	CGCGTTTTTA	GACGGTGCGT	TCATCCCCTG	TTTACTAGGG	540
GTTTTTGCTT	ACGCTTTAAG	AAAACGCTAT	TTTAAGAGCG	CGATCTTTGC	TTTGGTGGTT	600
TTAATTGTGA	ATACCGCTCT	TTTTAGTGGG	GATTTTAAATA	AAGGCTTGCC	TAGCGGGTAT	660
TTTATAGACA	CTTGCTTAGA	ACTCATGCTT	TGTATTCGCG	CCTTATTGTT	CCTCTACTAC	720
CCTTATACGC	TCTATAAAGC	CCTTTTGGAT	AAAAAGCCAT	CGTTACTAGC	CTTTATGGCG	780
CGAGCGGCTG	GCTTTTCCCT	TTGCTTTT				807

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090

AGCCCTTTTA	TGGATAGAAA	ACTCTTAAGA	TTATACCAGC	CCTTAAACGC	TTATTCTTAC	60
AATAGCGATT	CGCTTTTTTT	ATACGATTTT	TCACGCCCTT	TTATCAAAAA	TAGCGGCGCG	120
ATTTTAGACA	TAGGCTCAGG	GTGTGGGGTT	CTAGGCTTGC	TCTGCGCTAG	AGACAACCCG	180
CTAGCGAGCG	TTCAATTTAGT	GGAAAAGGAT	AGCAAAATGG	CGTTTTGCTC	CCAAAAAAC	240
GCCCTTAAAT	TCCTAACGC	TCAAGTGTTT	GAGAGCGATT	TTTAGATT	TAACCCCTCCG	300
ATTTGTATG	ATGCGATTGT	GTGCAACCCT	CCTTTTATG	CTTTAGGATC	TATTAAATCT	360
CAATTAAG	GGCATGCGAG	GCACCAGAGC	GAATTAGACT	TCGCTTCTTT	GGTGGCTAAA	420
GTGAAAAAT	GCCTGAAACC	TAAAGGGTAT	TTTATTTTTT	GCTATGAAGC	CTTGTGCTT	480
TGCTTGCTCA	TAGAGAGCTT	AAAAAGCGTT	AAACTCACGC	TAGAACTTT	AAGGTTTGTG	540
CAAAGTTCA	AAGACAAAA	CGCCCATTTG	ATGCTTGGAG	CGGCTAGGAA	TAATTCCAAA	600
AGCGCTCTAA	AAGTTTTGCC	CCCTTAATC	ACGCACAATT	CCAAAAACCA	AAGCGACAAC	660
ACCAAAGAAG	TTTAAACAT	CTATCAAAT	TGTAACACTT	ATTCTATCAA	AGCGCCTTA	720
GAT						723

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091

TCTCGTTCCT	TTAGGGGGCT	ATTATATTAT	AATAAGATAA	ATTTGATTAA	TAAGGATACA	60
GGCTTGCAAG	AAATTAAATT	AGACATTAT	GCCACTTTAG	TGTGCATGGT	TTTGGTGTTG	120
CTTTTGGGGC	GTTATGTGAT	TTCTAAAGTC	AAGTTTTTAA	GAGATTATGA	TATTCCAGAG	180
CCTGTTGTGG	GTGGGGTTTT	AGTCGTTTTT	TTTATCATGT	TAGCGCGTCA	ATTTTATCAT	240
TTTGGCTTGC	AGTTTGATTG	TTCTTTAAAA	GATCCTTTAA	TGCTGACTTT	CTTCATCACC	300
ATTGGTTTGA	GCGCGGATTT	CAAATCTTTA	CAAAAAGGCG	GGAAAATGCT	TGCGGTTTTT	360
TTGCTGGCTG	TAGCGGGGTT	TGTGGTGTGC	CAAAATGCAG	TGGGGATTTT	TATCGCTAGC	420
CTTTTAGGGG	TCAATCCTTT	AATGGGGCTT	TTAGGGGGAT	CGATCGCTTT	AGTGGGTGGG	480
CATGGCACTA	GTGCGGCATG	GGCTAATTTT	TTACCCCAAC	CACCTTATCA	TTTTAGCTCT	540
AGCTTGGAAG	TGGGCATGGC	GTGCGCGACT	TTTGGCTTGG	TGAGCGGGGG	GATTATTGGA	600
GGGCTGTGCG	CTAAATATTT	GATTTCTAAA	TACAAACTAG	AACCTAAAGA	CACTAAAGAA	660
AAAGACACTT	TAGAGGGCGT	GGTGTCTAAA	GGTTTTGAAA	CCCTTAAAGA	GCAGCGCCTA	720
ATCACTGTCAT	CCAGTTTTGT	AGAACTTTTA	GCTCTCATGT	CAATAGCTTT	ATTAGTGGGG	780
ACTTTTTTAT	CGCATTTGAT	GCCTAAAAGT	TTACCTTAC	CGACTTTTCT	GTGGTGTTTG	840
TTTGTGGGGG	TTATCTTAAG	GAACGCTTTG	TGTTTTTTTA	AAATCCATAG	CGTGTTTGAC	900
AGAGAGGTTT	CAGTTATAGG	GAATGTGAGC	TTGAGCCTGT	TTTAGCTTA	CGCTTTAATG	960
AGCGTGAATT	TATTGGAATT	GTTAAACTC	GCTGTGCCTT	TAGCGGTTAT	TTTGAAGGTT	1020

SUBSTITUTE SHEET (RULE 26)

796

CAAGTGGCCG	TTATGATCCT	TTATGTGGTG	CTTGTAACCT	TTAGGGTATG	CGGGAAGGAT	1080
TATGATGCGG	CGGTGTTGTG	CGCGGGGCAT	TGCGGTTTTG	GGCTTGGAGC	GACCCCAACG	1140
GCTATGGTGA	ATATGCAAAC	CATCACCAAC	CACTATGGGC	CATCGCATGT	GGCGTTTATC	1200
GTCGTGCCTT	TAGTGGGAGC	GTTTTTGT	GATATTATTA	ACGCTTTAGC	GATTAAAGGC	1260
TTTTTGCTTT	TGCCTTTTTT	CCCTAGT				1287

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092

AAATTCGTTT	TGCGTTCAAT	TTCAAGGATA	AAGATGCTTT	CAGTGTATGA	AAAAGGGAAT	60
GCCCTAGACA	AAAGGGTGCT	TGAAGAATGG	CTTTTAAGCG	AAGACATTTT	AATGGAAAAC	120
GCCGCTATGG	CTTTAGAAAG	GGCGGTTTTA	CAAAACGCTT	CTTTGGGCGC	TAAGGTCATT	180
ATTCTTTGTG	GGAGTGGGGA	TAATGGAGGT	GATGGCTATA	CTCTAGCCAG	GCCTTTAGTG	240
GGGCGTTTTA	AAACGCTGGT	CTTTGAAATG	AAATTAGCAA	AAAGCCCCAT	GTGCCAATTG	300
CAAAAAGAAA	GGGCTAAAAA	AGTAGGGGTA	GTCAATCAAAG	CATGGGAAGA	AAAGAATGAA	360
GATTTAGAAAT	GCGATGTGTT	AGTAGATTGC	GTGTTAGGGA	GCGCTTTTAA	GGGCGGATTA	420
GAGCCGTTTT	TAGATTTTGA	AAGCCTTTCT	CAAAAAGCAC	GCTTTAAAAT	CGCTTGCGAC	480
ATTCCTAGCG	GGATAGATTG	TAAAGGCAGG	GTGGATAAGA	GCGCTTTAAG	GCGGATACGA	540
CTATCAGCAT	GGGCGCTATC	AAGTCATGCT	TAC			573

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093

SUBSTITUTE SHEET (RULE 26)

797

AATGCCCACA	ACTTGAAAGA	TAAAACCTTT	CAGGGGGGGT	TTGAACTTCT	TACGACCCCC	60
AAAGAATACT	CATGGTGTGG	GGTTGTTTTA	AGCCTTTTGT	TGGCGATTAA	CCTTTATTTA	120
GAATACTTGA	ATCACC AAAA	GCTTGATTTT	TCAAAACCTA	CAAGCTTGAA	CGCTCAAATC	180
TTATTACAAT	ACCCTAAAAC	GAAAGATCAA	AAAACCTATT	TTGTCTTAAA	ACTCCAATCT	240
AAGGGCATGA	TCTTTTACAC	CACCATTAAA	GAGCCTTTAA	AAAACCTCCA	ATACCGCTAT	300
GCGCAATTTT	TTGGCAAGAT	CAAGCCTTGT	TCGTTCTTAG	AGTCTCTAAA	ATCATGCTTT	360
TTTCAAACCT	ATTCTTTTTC	TTTAACGCGA	AAACAAGATT	TCAAATCGCA	TTTGCGCCAT	420
TTCAITGACA	GCGCCCATTC	CAACGCCTTA	GTGGGTAATT	TGTATCGAGC	GTTATTCTATA	480
GGGGATAGCT	TGAATAAAGA	CTTAAGAGAC	AGGGCTAACG	CGCTAGGGAT	CAACCACTTA	540
CTGGCCATTA	GCGGGTTTCA	TTTAGGGATT	TTGAGCGCGA	GCGTGTATTT	TCTTTTCTCT	600
CCTTTTATATA	CCCCCTTACA	AAAACGCTAT	TTCCCTTACA	GGAACGCTTT	TTATGATATA	660
GGGGTTTTGG	TGTGGGTTTT	TTTGCTGGGG	TATTTATTGC	TATTAGATTT	TTTACCCTCT	720
TTTTTCAGGG	CGTTTTTAAT	GGGCTTATTA	GGGTTTTTGG	CATGCTTTTT	TGGGGTAAGG	780
ATTTTGAGTT	TTAAACTTTT	GGTTTTAGCG	TGCTGTATCG	CCATAGCGTT	ACTCCCTAAA	840
TTGCTTTTTA	GCGTGGGGTT	TTTGCTTTCT	GTTTGTGGGG	TGTGGTATAT	CTTTTTGTTT	900
TTAAACACACA	CTCAAAATTT	TTTTAAAGAT	TCTTCTTTTT	TCAAGCGATC	GTTTCAAGCG	960
ATCGCTTTAA	GCGTGTTAGT	GTTTTTGAAC	ATGCTCATTG	TTGCGCATGC	CTTTTTCCCT	1020
ATGTTTTTCGC	CCTACCAGCT	CTTTAGCATT	CCTTTAGGCT	TGATTTTTAC	TGTGTTTTTC	1080
CCTTTGAGCT	TGTTCTTGCA	TGCGGTGGGT	TTAGGGTCTT	TATTGGATAA	TATTCTAAGC	1140
ATGCCTTTAA	CCATCCCCAC	GATTTTCGGT	TCTTCGCCCT	TATGGCTTTT	GGGGGCGCAT	1200
TTGTTTTTAA	CGATTTTAAG	CGTGCGTTTT	TTTAAGGTTT	ATTTAAGCAT	GAATGTTTTG	1260
AGCATGGGCT	TTTTCTTGTA	TTGTTGCTAT	CAATATATTA	TAATGCCTAG	TTTAATTGTG	1320
GGT						1323

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094

GAGGCGTTTA	AGGCGGATAC	GACTATCAGC	ATGGGCGCTA	TCAAGTCATG	CTTACTAAGC	60
GATAAGGCTA	AAGACTATAT	AGGGGAATTG	AAAGTGGGGC	ATTTAGGGGT	TTTTAATCAA	120
ATTTATGAGA	TCCCAACAGA	CACTTTTTTA	CTAGAAAAAA	GCGATTTGAA	ACTGCCCTTA	180
AGGGATAGAA	AAAACGCTCA	CAAAGGCGAT	TACGGGCATG	CGCATGTGCT	TTTGGGCAAG	240
CATAGTGGGG	CGGGGTGTGT	GAGCGCTTTA	AGCGCGTTAA	GTTTTGGATC	TGGGGTGGTG	300
AGTATCCAAG	CGTTAGAGTG	CGAGATAACT	TCTAATAACA	AGCCTTTAGA	ATTGGTTTTT	360
TGTGAAAATT	TCCCTAAAAA	GCTCAGCGCG	TTCGCTCTTG	GCATGGGGTT	AGAAAAATATT	420
CCAAAGGATT	TTAAGAAGTG	GCTTGAATTA	GCCCCATGCG	TTTTAGATGC	GGGCGTTTTT	480
TATCATAAAG	AAGTGTTACA	AGCCTTAGAA	AAAGAAGTGA	TCTTAACCCC	TCACCCCTAAA	540
GAGTTTTTAT	CGTTATTGAA	ATCAGTGGGG	ATCAATATAA	GCATGCTAGA	ATTACTAGAC	600
AATAAACTAG	AAATCGCAAG	GGATTTTTCT	CAAAAATACC	CCAAGGTGGT	TTTGCTTTTA	660
AAGGGGGCTA	ATACCCTAAT	CGCTCATCAA	GGGCGGGTTT	TTATCAACAA	TTTAGGGAGC	720
GTGGCTTTAG	CCAAAGCAGG	CAGTGGCGAT	GTGTTAGCCG	GGCTGATTGT	AAGCCTACTT	780
TCTCAAAACT	ACACGCCTTT	AGACGCCGCC	ATTAACGCAA	GTTTGGCGCA	CGCCCTAGCG	840
GGTTTGAAT	TTAAGAATCA	TTACGCTTTA	ACGCCCTTAG	ATTTGATAGA	AAAGATCAAA	900
CGACTA						906

SUBSTITUTE SHEET (RULE 26)

798

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095

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CTCGCTTTAG CGTCAAAAGC GACCGGGTTT CCCATTGCAA AAGTGGCTAC CATGCTTGCG      60
GTGGGTTTTA GCTTAGATGA AATTAAAAAC GATATTACCA ACACCCAGC GAGCTTTGAG      120
CCTAGTTTGG ATTATATCGT GGTGAAAATC CCTCGCTTTG CGTTTGAAAA ATTTGCCGGT      180
GTTTCTAGCA CTTTAGGGAC TTCCATGAAA AGCATTGGAG AAGTGATGGC GATAGGGGGG      240
AATTTCCTAG AAGCCTTACA AAAAGCGTTA TGCTCTTTGG AAAACAATTG GCTAGGGTTT      300
GAATCGTTAA GCAAAGATTT AGAGGCGATA AAAAAGGAAA TCCGCCGCC CAATCCCAA      360
CGCTTGCTCT ATATTGCTGA TGCCTTCAGG TTGGGCGTTT CTGTGGATGA AGTGTTTGAA      420
TTATGCCAGA TTGACAGGTG GTTTTATCT CAAATTCAAA AACTAGTCAA AGCAGAAGAG      480
GGCATCAATT CTAGCGTTTT AACGACGCC AAAAATTGA GAGGGCTTAA AAATTTAGGC      540
TTTAGCGATG CCAGGATTGC CACTAAAATC AAAGAAAATG AAAATTAGA GGTACGCCCT      600
TTTGAAGTGG AATTAGCTAG ATCTAATTTA CAAATCGCGC CCCATTTGA AGAAGTGGAC      660
ACTTGCCTGG CGGAGTTTTT ATCGCTCAGC CCTTATTTGT ATTCCACCTA TGCCCCTAAC      720
CCTTTGCCCC CTATTGGAAA CAAACAAGAA AAACAAGAAA AGAAATCCT AATCATAGGC      780
TCTGGGCCTA ACCGCATCGG TCAAGGCATT GAATTTGATT ATTGTTGCGT GCATGCGAGC      840
TTTGCTTTAA AAGATTTTGA CATTAAAAGC GTCATGCTCA ATTGCAATCC AGAAACCGTA      900
AGCACGGATT ATGATACTAG TGATACGCTC TATTTTGAAC CCATACATTT TGAATGTGTG      960
AAGAGTATCA TTCAAAGGGA GCGAGTGGAT GGCATTATCG TGCATTTTGG GGGACAAACC     1020
CCTTTAAAC TCGCTAAAGA TTTAGCCAAA ATGCAAGCCC CCATTATTGG CACGCCTTTT     1080
AAGGTGATTG ATATTGCAGA AGACAGAGAA AAATTTCCCT CTTT                      1125

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(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...456

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096

CGTCCAGTCA	TTAGCGCCAA	AGAAGGGAGC	GATCCAAGCT	CTCTAGCTTA	CAACACCATA	60
GAAAGCGCGA	TCGCTAAAAA	TATAGATGAA	GTTTTTATAG	ACACCGCCGG	GAGGTTGCAC	120
AACCAGACCA	ACCTCAAAAA	CGAGCTTTCT	AAAATCGCGC	ACACCTGCTC	TAAAGTTTTA	180
AAAGACGCCC	CCTTTTACAA	ATTCTTTATT	TTAGACGGCA	CGCAAGGGAG	TTCTGGGCTA	240
ACGCAAGCGA	AGATTTTCCA	TGAGACTTTG	GCGCTAGATG	GCGTGATTAT	GACTAAGCTT	300
GATGGCACTT	CTAAGGGGCG	AGCGATTTTA	AGCGTGCTGT	ATGAGTTGAA	ATTACCCATT	360
CTTTATTTAG	GAATGGGCGA	AAAAGAAGAC	GATTTGATCG	CTTTTGATGA	AGAACGCTTT	420
ATAGAAGATT	TGTTTGATGC	GGTGTGTTG	GAACAA			456

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic).

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097

AATTTAAGGA	TTATAACCAT	TAAAACGATT	TTTAGAGATT	TTTGTAAGA	ACGCTTGAAA	60
AGGGCTAAAT	CAAAAAATAA	AGTCAGGGAT	AAATTGGGCTT	GCAAGCTTTT	GTTTTGGAAA	120
CTCAAGATT	ATCAAAATAT	TTTATTGTAT	AGCCCATTAG	GGCATGAGCT	TGACATTAGG	180
CCTTTGATTT	TGAAGTTAAG	ACAAAAAAT	AAGCGCGTGT	GTTTGCCTAA	AAGCATCAAA	240
AAAGGCGCTC	ATTTTTCTAA	AGAGGGTTTT	ACTATCGCGC	CCTTTAGGTT	GCCATTAAGG	300
CGTTTGGGGT	GTTTGATGA	GCCGAGTTTG	TCGCGCTATT	ATAAGCGGGA	ATTGGATTGT	360
ATTGTCGTGC	CGATTTTAGG	AATGGATACA	AGCTTTAGGC	GCGTGGGTTT	TGGGCTAGGC	420
ATGTATGATA	GGAGTTTACC	CCAATTATTC	AAAAAGCAAC	TAAAACGCCC	CTTAGTCATA	480
TTTGTAAGTA	GGGAGTTAGC	GCTGGCTAAT	GGTATTCTTA	CAGACGCCTA	TGACATTGAA	540
GCAAAATCTTT	ACATGAATGC	TCGTATCGTT	ATGAAGAATA	ATAAAAGGAA	ACATTATGAG	600
CAGCGGGTTA	ATTACATTT	CATTAGAAGT	CTTGCTAGCG	TGTTTGATCA	CCGCTCTAAT	660
CATGTATTAT	GTGATGAAAA	AGATCTATTA	CGC			693

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

800

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098

AGAATAATAA	AAGGAAACAT	TATGAGCAGC	GGGTAAATTT	ACATTTCATT	AGAAGTCTTG	60
GTAGCGTGT	TGATCACCGC	TCTAATCATG	TATTATGTGA	TGAAAAAGAT	CTATTACGCT	120
AGAGGGCAAG	CCATTTTAAA	AGGCGCTTCA	GCCAAAGCTA	AATTAATGGA	ATTTCAAGCG	180
AAATCTTTTC	TGGAAGCTGA	AGAAATGCGC	ATGAAAAGCC	AAGAAATGCA	GTTGCAACAG	240
CAATATGAAA	ATAAGAAATT	GCAACTCCAA	ACCCATTTTG	ATAAAAAAGA	AGCGCATTTG	300
AAGCATTTAG	AAGCGCAGCA	CAAAGAATTT	GTAAGAGATG	AAAAACGCTA	TTTGGAAAAG	360
GAAAAAAAAG	AGCTTGAAAA	AGAACGCCAA	ATTTTAGAAC	AAGAGAGGGA	AAATTTTAAA	420
AAACAGCGCG	CCATTTGTAA	AGAAGCTCAA	GCCAAAGCGC	TAGATGCGAT	GCTCAATTAC	480
ATGGCTTATA	CCAAAGATGA	AATTAAGAGC	ATGATCTTAG	AGCAATTAGA	ACAGGAACTA	540
GAAGCGCAAA	AGAGCGCCTT	GATCAGGCGT	TATGAAGAAG	AAGCCTTTAT	TATGTGTTTA	600

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099

ATAAGGTCAT	CAATGACAC	CCAAACCACC	CAAACACCAT	GGCACTCAAA	CACCAGACGG	60
CCAAAACCCA	CCCCTAAACC	CATTAAAAAA	GAGGCTAAAA	AGGCTAAAGA	GAAAAACAACT	120
AAGCATGCGC	ATTCAAAGCA	TGCGCACTCT	CCATTGAACG	AAAGGAGCGC	TAAAAAAGAA	180
ATTCCCTAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	240
ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAAA	AAGAAATCCC	TAAAAAAGAA	300
GCAGAAAATG	AGAGTAAGAA	CCAAATCTTT	ATAGCAGAAA	AAAATGATAC	TTGGATCAAA	360
ACCAAGCGCA	AAAAACACAA	AAAGATCGTT	TTGGACGCTG	GGCATGGGGG	GAAAGATTGC	420
GGGGCGATGA	GCGCGAATTT	GGTGTGTGAA	AAGGACATTG	TTTTAGAAGT	GGTGAAGTTT	480
TTGCATAAAG	AGCTTAAAAA	AAGAGGCTAT	AGCGTTTTAT	TGACAAGGGA	TAAGGACATT	540
TACATTGATT	TAGTGGCCCG	AACGGAATTA	GCCAAATAAA	AAGGGGCGGA	TTTATTTCATC	600
TCAGTGCATG	CCAATTCCAT	CCCTAAACGC	TCCACCTCTA	ACGCCCATGG	CATAGAGACT	660
TATTTTTTAT	CCACCGCAAG	GAGTGAAAGG	GCTAGGAAAG	TGGCTGAGCA	AGAAAATAAA	720
GACGATGTGA	ATTAAATGGA	CTATTTTTCT	AAAAGTTTGT	TTTTAAATTC	ATTGAACACG	780
CAGCGATTGA	TCGTCTCCAA	CAAATTAGCG	ATTGACGTGC	AATACGGCAT	GCTCCAAAGT	840
GTCCGCAAAA	ATTACCCTGA	TGTGGTGGAT	GGGGGTGTTA	GGGAGGGGCC	TTTTTGGGTG	900
TTAGCCGGGG	CTTTAATGCC	TTCAATTTTA	ATAGAAATTG	GTTATAATTC	CCATGCGATA	960
GAATCTAAAC	GCATCCAAAG	CAAACCGTAT	CAAAAAATCT	TGGCTAAGGG	CATTGCTGAT	1020
GGCATTGATA	GTTTCTTCAG	CAAGAATGAT				1050

(2) INFORMATION FOR SEQ ID NO:1100:

SUBSTITUTE SHEET (RULE 26)

801

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100

AGAGTATCTA	TGAATGTCAA	AAAAAAGGGA	AAGCCACAAA	GTGGAAGAT	TGATAGGGTG	60
GATTGTTTGG	AGAAACTTGG	GAAAGAAAAC	ACTACTTTTT	TAAGCAGTAT	AGCTATGGGG	120
AGCATTTGGC	AATTAGCGAT	CCCCATTCCCT	GGAGTTGGAG	TGCTCATTGG	GGGCTTTGTG	180
GGTGGGGTGA	TGAGTAAAC	TTTTTATGAT	GTCTCGCTAA	CGATTTTCAA	AGAGGCTAAA	240
TTAGCCGGTC	AAAGGCGTAT	TGAGATTGAA	AAAGAATGCC	GTGAGAGTAT	CAGACAGTTA	300
GAGATGTATC	AAAATCAATT	TAATGAAGTG	TTTGAGCGGT	ATTTTCATGG	GACTATAAAA	360
TTCTTTAATG	AAAGTTTGA	TGAGCTGGAG	AGGGCGCTTT	GTGCGGGCGA	TGCGGATTG	420
GCTATAGCAG	TCAATAACAA	GATCCAAGAG	GGGATGGGTC	AAGAGTTGCT	GTTTGACAAT	480
AAGCAAGAGT	GCTGGGAATT	TATCACTAGC	CGTAAAGAGG	GTTGGAATTT	CGTCACTAGC	540
CGTGGAAAAA	CAGAAATT					558

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1086 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101

AAGAGGGATC	AAATGGCCGA	AGAAGAAAAG	ACCGAACTCC	CTAGCGCGAA	AAAAATCCAA	60
AAAGCCAGAG	AAGAAGGCAA	TGTGCCTAAA	AGCATGGAAG	TGGTGGGGTT	TTTAGGGTTA	120
TTGGCTGGGC	TAATGAGTAT	TTTTGTTTTT	TTTATATGGT	GGGTGGATGG	CTTTAGCGAG	180
ATGTATCGCC	ATGTGTTGAA	AGATTCTCC	CTAGATTTTA	GCAAAGAAAAG	CGTTCAAGAG	240
CTGTTTAACC	AGCTGGCTAA	AGACACTTTT	TTATTGCTTT	TGCCTGTTTT	AATCATTTTA	300
ATGGTGGTGG	CGTTTTTGTC	TAATGTCTTG	CAATTGGCT	GGCTCTTTGC	CCCTAAAGTC	360
ATTGAGCCTA	AATTTTCTAA	AATCAACCCT	ATCAATGGCG	TCAAAAACCT	TTTTTCTTTA	420
AAAAAGATCC	TTGATGGGAG	TTTGATCACT	TTAAAAGTTT	TTTAGCTTT	TTTCTGGGG	480
TTTTTCATCT	TTTCCTTATT	TTTAGGGGAA	TTAAACCATG	CGGCTCTTTT	GAATTTGCAA	540

SUBSTITUTE SHEET (RULE 26)

802

GGCCAGTTGT	TGTGGTTTAA	AAGCAAGGCG	TTATGGCTCA	TTTCTTCGCT	TTTATTTTAA	600
TTTTTTGTCT	TGGCTTTTGT	GGATTTAATC	ATCAAACGCC	GCCAATACAC	TAACCTTTTA	650
AAAATGACTA	AACAAGAAGT	TAAGGACGAA	TACAAACAGC	AAGAAGGAAA	CCCAGAAATC	720
AAAGCCAAAA	TCCGCCAGAT	GATGGTAAAA	AACGCCACGA	ATAAAATGAT	GCAAGAAATC	780
CCCAAATCCA	ATGTCGTGGT	GACTAACCCT	ACCCATTATG	CCGTCGCTCT	CAAATTGAT	840
GAAGAACACC	CTGTGCCTGT	GGTAGTGGCT	AAAGGCACGG	ATTATTAGC	CATTAGGATT	900
AAGGGTATCG	CCAGAGAGCA	TGACATAGAA	ATTATAGAAA	ATAAACGCT	CGCTAGAGAG	960
CTTTATAGAG	ACGTGAAAT	GAACGCCACC	ATACCAGAAG	AATTGTTTGA	AGCGGTAGCG	1020
ATTGTCTTCG	CTCAAGTGGC	TAAATTAGAG	CAAGAACGCC	AAAAACAAAA	GATCATTAAT	1080
CCTCTT						1086

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102

GAAAATACTA	TGCAAGATTT	ACAACATTTT	AAAAATGATA	TTACGCTCAT	TCTGTCTAAA	60
GACAGATTAG	ATACTTATGA	CAGCCTAGAG	CAATACAAAG	AAAAATTAAA	ACTCATTCT	120
TTCATCAGCG	CTAAATCTC	TAACCTAGAG	ATTTATTTAC	GCAACGCTTT	AGACTATTGC	180
TTAACCCTAA	TTAAGGGGAG	CGAATGGGTG	TTAATGAAA	ATTCTTTAAC	AGATTTAATT	240
AACGAACAAA	AAGAAAAGAA	AAAAGAAATC	ACGCATTCTT	TAATCTTATC	TAAAATGTCT	300
TTAGGGGCG	TGGTTAGGCT	TATTTTGT	TATAAGTTAG	AGGGGGTAAT	ATTAGATTG	360
AGAGCGTATC	GTTTGAAGAGC	TTATTATCAC	GAAAATAAAG	ATACCTTGCT	TATTAAAGGC	420
AAAAAACGCC	TTCTTTACAA	TTATATTAAA	GCCCATATTG	CTTTAAACTT	GCTATGGACA	480
ATTAGAAATC	GCACGTATCA	TTGGGAAAAT	TTACTCAAAA	TCCAACCGAA	CAACCGCCCA	540
CAA						543

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

803

(A) NAME/KEY: misc_feature
(B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103

GCTAATGGAT	GCGAAAAAAG	GATTTTCATG	CTGCTTTGCG	CGGGAAGGAA	TGAGACTTTA	60
AAAAAAGCGG	TGCCTATTGG	TGTGGGCTTG	ATAGAGAGCG	CGATCAATTT	AACGAGAATG	120
TGCCTTAAAA	ACCCTGATAC	AGAAAGCCTT	ATTTTATAG	GGAGCGCGGG	GAGTTATAGC	180
CCAGAAACGG	AGATTTTGAG	CGTGTGTGAA	AGCATTGAAG	GCTATCAAAT	TGAAGAGAGT	240
TTTAGCCATT	TAAACAGCTA	CACGCCTTTG	GATAATTTCA	TTCACATAGA	AACTAAAGAG	300
CAGGCTCTTT	TTGAAAGGGT	GCGTGTGAAT	AGCAGTAACT	ACATCCACAC	CAGCGAAATG	360
TTTGCTAAAA	AAATGGTTCA	AAAGGGCGTT	TTATTAGAAA	ACATGGAGTT	TTTtagCGTC	420
TTAAGCGTGG	CTAAAATTTT	TTCTTTAAAG	GCTAAAGGGA	TTTTTTGCGT	GAGCAATCAT	480
GTAGGGCTTA	ACGCGCATAA	GGAATTTAAA	GAAAACCACG	CCAAAGTCAA	ACAGATTCTA	540
GAAACATCA	TTGATAGTTT	GATAGTT				567

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1018 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104

TTTTAATGAG	TTTTATAAGC	TTGCAATCGC	CTCTTGGCAA	GAACCCTTAA	GAGTGAGTAT	60
AGAATTTGTG	GATTTGCCTA	AAAAAATCAT	CCGTTTTCCG	GCCCATGATT	TGAAAGTGGG	120
GGAGTTTGGT	TTTGTGGTTA	CTCAACTTTC	AGATTATGAA	ATCGTTAATT	CTGAAGTGGT	180
CATTATTGCT	GTTGAAAATG	GCGTCGCAAC	GGCTAAATTC	AAAGCGTTTG	AGTCGATGAA	240
ACAAAGCCAT	TTACCCACTC	CAAGAATGTT	CGCTAAAAAA	GGGGATTAG	TCTATTTTCAG	300
GCAATTTAAC	AACCAAGCGT	TTTTGATCGC	TCCTAATGAT	GAAGTCTATG	AGCAAATCAG	360
AGCGACTAAC	ACCGATATTA	ATTTCATTAG	CTCTGATTTG	TTGGTTACTT	TTTGAATGG	420
GTTTGACCCA	AAAATCGCTA	ATTTAAGGAA	AGCGTGCAAT	GTTTATAGCG	TGGGGGTGAT	480
TTATATTGTA	ACCACCAACA	CGCTCAATAT	TTTAAGTTGT	GAGAGTTTGT	AAATTTTAGA	540
AAAAAGAGAG	CTGGATACAA	GCGGCGTTAC	TAAAACTTCC	ACGCCGTTTT	TTTCTAGGGT	600
TGAGGGCATT	GATGCAGGCA	CGCTAGGGAA	ACTTTTTTCA	GGCAGTCAAT	CTAAAAATTA	660
CTTCGCTTAC	TATGACGCTT	TAGTGAAAAA	AGAAAAACGA	AAAGAAGTAA	GGATTGAAAA	720
GAAAGAAGAA	AGGATTGATG	CTAGAGAAAA	TAAACGAGAA	ATCAAGCAAG	AAGCCATTAA	780
AGAGCCTAAA	AAAGCCAATC	AAGGCACAGA	AAACGCTCCC	ACTTTAGAAG	AGAAAACTA	840
CCAAAAAGCA	GAGCGAAAAT	TTGACGCTAA	AGAAGAAAGG	CGTCGTTCAA	GAGATGAAAG	900
GAAAAAAACT	AAAGCCACCA	AAAAGGCTAT	GGAATTTGAA	CAAAGAGCGA	GAGAACATCA	960
AGAAAGAGAT	GAAAAAGAGC	TTGAAGAAAG	AAGAAAAGCT	TTAGAAATGA	ATAAGAAG	1018

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

804

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105

GGAGAAACAA	CAATGAACT	GAGAGCAAGT	GTTTTAATCG	GTGTGGCAAT	TCTGTGCTTA	60
ATTTTAAGTG	CGTGCACTAA	CTATGCGAAA	AAAGTGGTGA	AACAAAAGAA	CCATGTTTAT	120
ACGCCTGTGT	ATAATGAACT	GATAGAGAAG	TATAGTGAGA	TCCCCTTAAA	TGACAAACTC	180
AAAGACACAC	CATTTCATGGT	GCAAGTGAAG	TTGCCAAATT	ACAAGGACTA	TTGTGTTGGAT	240
AATAAACCAAG	TTGTACTAAC	TTTCAAACCT	GTTCCACCATT	CTAAAAAGAT	TACGCTCATA	300
GGCGATGCCA	ATAAGATCCT	CCAATACAAG	AATTACTTCC	AAGCTAACGG	GGCAAGATCT	360
GACATTGATT	TTTACTTGCA	ACCCACTTTG	AATCAAAAGG	GTGTGGTGAT	GATAGCGAGT	420
AACTACAATG	ATAATCCCAA	CAACAAAGAA	AAACCACAGA	CCTTTGATGT	GTGCAAGGA	480
AGTCAGCCAA	TGCTAGGAGC	TAACACAAAA	AACTTGCAATG	GCTATGATGT	GAGTGGAGCA	540
AACAACAAGC	AAGTGATCAA	TGAAGTGGCA	AGAGAAAAAG	CTCAGCTAGA	AAAAATCAAT	600
CAGTATTACA	AGACTCTCTT	GCAAGACAAG	GAACAAGAAT	ATACCACTAG	GAAAAATAAC	660
CAACGAGAAA	TTTTAGAAAC	ATTGAGTAAT	CGTGCAAGTT	ATCAAATGAG	GCAGAATGTG	720
ATTAGTCTCG	AGATTTTAA	GAATGGCAAC	TTGAACATGC	AAGCCAAAGA	AGAAGAAGTT	780
AGGGAGAAGC	TACAAGAAGA	AAGAGAGAAT	GAATACTTGC	GCAATCAAAT	CAGAAGTTTG	840
CTCAGTGGTA	AG					852

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106

AGTTATTGTC	AAATGAAAAC	ACTCGTGAAA	AATACCATAT	ATTCTTTTTT	GCTATTGTCT	60
GTTTTGATGG	CAGAAGATAT	AACAAGCGGC	TTAAAGCAAC	TGGATAACAC	CTACCAAGAG	120
ACCAACCAAC	AAGTGCTCAA	AAACCTAGAT	GAGATTTTTT	CAACCACTAG	CCCTAGCGCT	180
AATAATAAAA	TAGGTCAAGA	AGATGCTCTA	AACATCAAAA	AAGCGGCCAT	TGCTTTGAGA	240
GGAGATTTAG	CGTTATTGAA	AGCCAATTTT	GAAGCGAATG	AGTTATTTTT	CATCTCAGAA	300
GATGTGATTT	TTAAGACTTA	TATGTCTAGC	CCTGAACTTT	TATTAACCTA	TATGAAAATC	360
AATCCCTTAG	ACCAAAAGAC	TGCTGAGCAA	CAATGCGGAA	TATCCGATAA	AGTTTTAGTT	420
CTTTATTGTG	AGGGGAAGCT	GAAAATCGAG	CAAGAAAAAC	AAAATATAAG	AGAGCGTTTA	480

SUBSTITUTE SHEET (RULE 26)

805

GAAACTTCTC	TAAAGGCATA	TCAGAGCAAC	ATTGGAGGTA	CAGCTTCCTT	AATCACTGCT	540
TCACAGACGC	TTGTAGAAAG	CCTAAAAAAT	AAAAATTTC	TCAAAGGAAT	CAAAAAGCTT	600
ATGTTAGCTC	ACAACAAGGT	CTTTTAAAT	TATTTAGAGG	AGTTGGACGC	ATTAGAAAGA	660
TCCCTAGAAC	AAAGTAAGCG	ACAATACCTA	CAAGAAAGGC	AATCAAGTAA	GATCATTGTT	720
AAA						723

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107

ATAAATAAGA	ACATGTTTAA	TATTAAGG	ACTTTTTTAA	TAACGATCAT	AAGTTTTTTT	60
CTCATGTTC	CTAATTGGTT	GAAAGCTATT	GATTTGCCCA	TTGTTTCAAA	TCTCAAAATT	120
TACCAAACAG	TTTATTGCAT	GCTGATACCG	AGTTATGTTT	TAACCAACAA	AAGTTTTGCA	180
GATATTTTGA	CAGGCTATAC	ATCTATTGGT	GCATCAGGGA	GTGGAAGAG	TTCAGGGCAG	240
GGTGTGATCG	AAGCGCTTAG	CACACCATTA	GCCACAAGTT	TAGCCGCTAG	CAATCTGGTG	300
AAATATTTGA	ATACTTTAGG	TCCTTTATGG	GGATCGGCGT	GGGCAAGTGT	TGCTACAGCT	360
ATACAAGGTT	TTGCTCTAAC	GCCATCAAGT	GGCTGTAATT	TTGGTTGGAA	CGCATTGATA	420
AATAAAAAACA	TAGATGTATC	CATGGATAGC	GTACTAGACA	ATTTGAGCAA	CAAGATTTCAG	480
AATTTTACCA	AAGCGGTGT	TGAGGACAAT	GTGAAAGGCA	ATATTCTTTT	ACAAATAATT	540
GGCTCAATAA	CCGCTCAAGC	TTCTACGAAT	ATTACAGCTG	ATGGTTTAAT	TTGGCTGATT	600
GGTAAAGAAT	TCACTGCAAA	TAACTGCAA	AACAACACTA	TAGCCATGCT	TGCTTTTGCC	660
GCATTAGAAT	CTGTTGTCAA	AGGAGCGGAC	GCTGCTGTTC	TTCTGCATA	TGGTGTAGTC	720
AATCTGCCTG	ATATTATCAT	AGGGCAAGGG	TCATATCTTG	ATTTTGTTTC	TTACCTAATT	780
TATATTGTTT	TTGGGATTIT	TGTTTTAIT	TCTTTTATGA	AATTGAGAGA	TATTTCAAAC	840
GGCATTTCAGA	TTAACATAGG	TTTTGAATAC	ATGCGATTTG	TTGGGGGGAC	ATTATTCAAA	900
ATGGCGATGG	TCTCTTTTAT	CGCCTATGCA	GGTTTGGTT	ATCTTTATAA	AATCTCTTAT	960
TCTATTIATT	TTGGTTTACG	AGGTGCTTTT	GGGCTGAATC	AAGTTCTTTT	TTGGGCTTTA	1020
GATTTAGTGC	TGAATTACAC	TGTTAATTCA	ATTTTACCTG	CGGTAAGAGC	TGTTTTTTCT	1080
AATGTTGGCA	ACAACGCTCC	TAGTTTGTTA	CAAGGCTTGC	AAGTGGCAGG	TATTTCTTTA	1140
TTGCTATTIT	TTATGCAAGT	AACTATCAIT	ATGAGAATAA	GCACTGTTGT	TGTGAAACCT	1200
TTGATAGCGG	GGGCTTTTAG	CGGTATTGTT	TTCCCTATTG	CAGTATGTTT	GATCGTGCTA	1260
GATTGGTTCA	AAGATTCTAT	GAAAAACATA	TTGATATGGT	TTATTAATAA	TCTGTTTATC	1320
TTGGTTCTAG	CTATTCCCTAT	TTTGCTCTTT	GGTGTTTTGG	CATTATGGGC	ATTCAATTG	1380
ACCATAACGC	CCTCTGTTGC	TATACAAAAC	ATCAATCAAG	GGGGATTGGG	TATCGATTCA	1440
ACTATTGCCA	GTITGATCAC	TCTATTIATT	TTAAAAGGTT	TCATAGAGAC	GATTATTGAG	1500
AGCGTCAATG	CGATCGTTAA	CACCATTTTC	AGCTCTGTCT	CTATGGATGG	TAGCAGAATG	1560
GATAGAGAAA	GAGATGCCTT	AATGGTGGA	AGAGTTGGTG	GATCTATGTT	TAAAGGA	1617

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

806

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108

CTCCATAGAA	TTATCTCCTG	CGATAGCGCT	TGGAGGACTA	ATCTTGTTGT	GCGGACCAAT	60
AAAGCCTTGT	ATCAATTCAT	TTTGAGGATA	GCCCAAAAAG	ACAATTTTGC	TTCAGCGTAT	120
CTAACAGTCA	AATTAGAATA	CCCACAAAGA	CACGAAGTCT	CTAGCGTTAT	TGAAGAGGAA	180
TTAAAAAGA	GAGAAGAAGC	AAAGAGGCAG	AGAGAATTGA	TCAAGCAAGA	AAATCTCAAC	240
ACCACAGCCT	ACATCAATAG	AGTAATGATG	GCGAGCAATG	AACAGATTAT	CAACAAAGAA	300
AAAATAAGAG	AAGAAAAACA	AAAAATTATA	CTAGATCAAG	CAAAGGCGCT	AGAGACCCAA	360
TATGTGCATA	ATGCGTTAAA	AAGAAACCCT	GTGCCTAGAA	ACTACAATTA	CTACCAAGCG	420
CCTGAAAAAC	GCTCTAAACA	TATTATGCCC	TCTGAAATTT	TTGATGATGG	CACATTCACT	480
TATTTTGTTT	TCAAAAACAT	CACTCTCCAA	CCTGCTATTT	TTGTGGTTCA	ACCTGATGGG	540
AAATTGAGCA	TGACTGATGC	CGCCATTGAT	CCTAACATGA	CTAATTCAGG	ATTGAGATGG	600
TATAGAGTTA	ATGAAATTGC	AGAGAAGTTT	AAGCTCATTA	AAGACAAAGC	CCTTGTAACA	660
GTGATCAATA	AAGGCTATGG	GAAAAATCCA	TTGACAAAAA	ATTACAATAT	CAAAAACTAT	720
GGTGAATTGG	AGCGTGTGAT	TAAAAAGCTC	CCTCTTGTCA	GAGATAAA		768

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109

ACTAGTTCTT	TCAAAACCAA	AATGAAACGA	CCGATCAGCA	AATTGAAACA	AAACTTTTTA	60
CAATTCAAAC	ATTCTTTCAA	CAAACATTTA	GATAAGTACA	GCCTTTATTA	TAGGCTGTTC	120
AATATCAGCT	CTATCGTTAT	AGGTTTTTTA	ATAGCGCTTT	TTTCTTATGG	GGCAGGGGTG	180
ATTTTAGTTT	ATCCAATATT	ATTCTTGTTT	GCTCTTATAA	TAAACCTAG	CTTTTTTTAT	240
TACACTACTT	ATCTTTTGCT	ACTCGTTTCT	CTCAGCATAA	TAAGCAAATA	CTATCTCCTA	300
AGCCACGCAA	ATTTCACAAT	GAAGCTAATC	ATGCTTATGA	CTCAATGGCA	AAATTGGTTC	360
TTA						363

(2) INFORMATION FOR SEQ ID NO:1110:

SUBSTITUTE SHEET (RULE 26)

807

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110

GTATGCTATT GTGAAATGCT TCCTACTAAA ACACGCATTA GAGATCCGAA CAAGCAAGAA	60
CTTACACAAC CAAAAATAAA AGGATTGAGT ATGGGAAAAA TTTTAGCTTC TTTGTTGGGT	120
GGCGGAACAA ATCTTTTAC AGGTTTATCC AGTGATTGT TTCTATGAT ATTAAATTTT	180
TTGTTCTTCC TGATGTTAAT GATGGGACTT AATGAAGCAT TAGGGAAAAA ATTTAACTTG	240
CCTATGGACA ATATCAAGAA TTTTATGGCA GAAGTGCTGA AGAATGGATT CGATAGTATC	300
AAAAACATGG GATCTGCTTT GGTGTTGTAAT GGTTTTGGTA GCAGCAAATC AGACAAAACC	360
ACTAATAAAA TGAGTGTCCC ACAAGTAAGA CTC	393

(2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 891 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111

GAGGAATTGT TGATGGGGCA GGCATTTTTT AAAAAAATG TTGGCTGTTT CTGTCTTGGT	60
TATTTATTTT TATCTAGCGC AATAGAAGCA GTAGCACTTG ACATTAAGAA TTTTAATCGT	120
GGTAGGGTGA AAGTGGTGAA TAAGAAGATT GCTTATTGG GAGATGAAAA ACCTATTACG	180
ATTTGGACTT CATTAGACAA TGTACCCTG ATCCAACTTG AAAAAGATGA AACTATTCTT	240
TACATCACAA CAGGTTTCAA TAAAGGTTGG AGTATTGTGC CTAATTCTAA TCATATATTC	300
ATTCAACCTA AATCGGTAAA AAGTAATCTC ATGTTTGAAA AAGAAGCAGT GAATTTTGCC	360
CTAATGACAA GAGATTACCA AGAATTTTAA AAGACAAAAA AACTTATCGT AGATGCGCCT	420
GACCCTAAAG AATTAGAGA ACAAAAAAA GCTCTAGAAA AAGAAAAAGA AGCTAAAGAA	480
CAGGCGCAAA AGGCACAAA AGATAAAGA GAAAAAAGAA AGGAGGAGCG TGCAAAAAAT	540
AGAGCCAATT TAGAAAACTT CACTAACGCT ATGAGTAACC CACAAAATTT GAGCAATAAC	600
AAAAATCTTA GCGAATTGAT CAAGCAACAG AGAGAAAAATG AATTAGACCA AATGGAACGA	660

SUBSTITUTE SHEET (RULE 26)

808

CTAGAGGACA	TGCAAGAGCA	GGCTCAAGCT	AACGCACTCA	AACAAATTGA	AGAGCTCAAC	720
AAGAAACAAG	CTGAAGAGGC	AGTTAGGCAA	AGAGCCAAGG	ATAAAATCAG	TATTAAGACA	780
GATAAATCTC	AAAAAAGCCC	CGAGGATAAC	TCCATAGAAT	TATCTCCTGC	GATAGCGCTT	840
GGAGGACTAA	TCTTGTGTG	CGGACCAATA	AAGCCTTGTA	TCAATTCATT	T	891

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112

AGCTGTCGCA	TGTTAGGGAA	AAAAACGAA	GAAGTCTTGA	TTGATGAAA	TTTGGTTGGG	60
GGTGTGATAG	CCCTTGATAG	ATTGGCAAAA	CTCAATAAGG	CCAATAGGAC	TTTCAAAAGG	120
GCTTTTTATC	TCTCTATGGT	GCTCAATGTC	GCCGCTGTAA	CGAGTATTGT	GATGATGATG	180
CCTTTGAAGA	AAACAGATAT	ATTTGTTTAT	GGCATTGATC	GATACACAGG	AGAATTTAAA	240
ATCGTCAAAC	GCTCCGATGC	TAGGCAAATC	GTCAATTCTG	AAGCCGTTGT	GGATAGTGCA	300
ACTTCAAAAT	TTGTCTCATT	GCTGTTTGGT	TATAGCAAAA	ATTCTTTGAG	GGATCGCAAG	360
GATCAACTAA	TGCAGTATTG	CGATGTGAGT	TTCCAAACCC	AAGCAATGAG	AATGTTCAAT	420
GAAAAATATCA	GACAATTCGT	AGATAAAGTC	CGAGCAGAAG	CTATCATTAG	CTCCAACATA	480
CAAAGAGAAA	AAGTCAAAAA	TAGTCCCTTA	ACGAGATTAA	CATTTTTTCAT	TACCATCAAA	540
ATCACGCCTG	ATACAATGGA	AAATTATGAA	TATATCACTA	AAAAACAAGT	AACTATTTAT	600
TATGATTTTG	CTAGAGGTAA	CTCTTCTCAA	GAAATCTTAA	TCATCAACCC	TTTTGGCTTC	660
AAAGTGTTTG	ACATTCAAAT	CACGGATTTA	CAAAACGAAC	AGACAGTAAG	CGAAATTTTG	720
AGAAAGATTA	AAGAAGTGGA	ATCAAAAAAT	AAGGCATTAA	ATAAA		765

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...750

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113

AAGCGCCTAA	TTCAAAGAGA	TGAGACAATC	GCAACTCAGA	GAGAGAATGG	TATAATATCA	60
AAACAAATTC	TCAATTTAAT	TCTTGAAAGG	AGTTTCATGA	ACGATACAAC	AGAGCACCAT	120
GGATCCAATC	CGCTAAACGC	CCCACCACCT	AGCAACTCAC	AGAGCAACGA	TCTCTTAAAT	180
TTGCTAGACT	CGTTATATCC	TAAAGGGAGT	TTAGGGGAAC	AAAGATTTC	CGAAGCTTTA	240
AAGAATCAAG	AAGAGTTGAA	AAATATCCTA	ATAGAAATAG	AAAAGCTACC	GCAAGAAAAA	300
AGGTATGAAC	TTCTGATGCA	GATAGGACAA	GCCAAACAGA	GAATAATGGA	AGCATACGCT	360
CATTCAATCT	TAGGATATAT	AGGGGGACTA	GAGCATCTGT	TAGGATTGTG	TATGGGTGGG	420
ATATTTGTTT	TGTTTGCAAT	CTATTTTGTA	TTTTTAAGAA	CTAGCAAAAA	CACAGAGCTA	480
GTGGAAGTC	TAAAAACAA	ATTAAAACTT	CAGTATTTTT	ACTATGCCTT	TGGTGTGGGT	540
GCGGTTTGT	TTTTTGGATT	AGAAACAATT	AGATCGATTT	ATGAAGTATA	TATCTTAGGA	600
ATTGGTAGCA	CTAACGACAA	GGTGCTCTTT	GTTTTGAAAA	ACATTTGCTT	CATAGGTATG	660
GGCTATTTGA	TTTATAAAGT	TATTAAAGTT	ATTGGTATAA	AAAATTTTAT	CAATGGTCTT	720
TTGCTTCAA	AGAAACAAGG	CGGTGCAGAA				750

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114

GGTTACAAAA	ACTATAAGAT	GCTTGCAAAA	ATCGTTTTTA	GCTCATTGGT	TGCGTTTGGA	60
GTTTTGTCGG	CTAATGTGGA	GCAGTTTGGT	TCATTTTTC	ACGAGATAAA	AAAAGAACAA	120
GAAGAAGTGG	CCGCAAAAGA	AGACGCTCTT	AAAGCTCGCA	AGAAGCTCTT	AAACAATACG	180
CATGATTTCT	TAGAAGACTT	GGTTTTTAGA	AAACAAAAAA	TCAAAGAGCT	TGTGGATTAC	240
AGAGCTAAAG	TTCTTTTAGA	TTTAGAAAAC	AAGTACAAAA	AAGAAAAAGA	GGCTCTAGAG	300
AAAGAGACAA	GAGGTAAAT	CCTTACTGCT	AAGTCAAAGG	CTTATGGTGA	TCTAGAGCAA	360
GCCTTAAAG	ATAACCTCT	TTATAAGAAA	CTTCTTCCTA	ACCCTTATGC	TTATGTTTTA	420
AACCAAGAAA	CATTCACGCA	AGAAGATAAG	GAGCGTTTGA	GTTATTACTA	CCCCAAGTG	480
AAAACGAGCA	GTATTTTTAA	AAAAACTACC	GCTACCACTA	AAGATAAGGC	TCAGGCTTTG	540
CTTCAAATGG	GTGTGTTTTC	TTTAGATGAA	GAGCAAAACA	AAAAAGCGAG	CCGATTAGCT	600
TTATCTTACA	AGCAAGCGAT	TGAAGAATAT	TCCAATAACA	TTTCTAATTT	ATTGAGCAGA	660
AAAGAATTGG	ATAATATAGA	TTATTACTTG	CAGCTTGAAA	GAAACAAATT	TGACTCCAAA	720
GCAAAAGATA	TTGCTCAAAA	AGCCACCAAC	ACGCTTATTT	TAACTCGGA	ACGCTTGGCG	780
TTTAGCATGG	CGATTGATAA	GATCAATGAG	AAATACTTAA	GGGGCTATGA	AGCTTTTTTCT	840
AACCTGTTGA	AAAATGTCAA	AGATGATGTG	GAGTTGAATA	CTTTGACTAA	AACTTTCACC	900
AATCAAAAAT	TGAGTTTTCG	ACAAAAACAA	AAATTGTGTT	TGTTGGTTTT	AGACAGCTTC	960
AATTTTGATA	CCCAATCCAA	AAAATCTATA	TTAAAAAAGA	CTAATGAATA	CAATATCTTC	1020
GTAGATAGCG	ATCCTATGAT	GAGCGACAAA	ACAACATATG	AAAAAGAACA	CTACAAGATA	1080
TTTAATTTCT	TCAAAACAGT	GGTTTCTGCA	TACCGGAACA	ATGTTGCCAA	GAATAACCCC	1140
TTTGAA						1146

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

810

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115

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AAATTTAGTG AAGTATATTT TATAATGAAA ACTAAGGCAG GCTTTGTAGC TCTTATAGGC      60
AAACCAAACG CTGGAAAAAG CACTCTTTTA AACACTTTAT TAAACGCTCA TTTAGCCCTT      120
GTTTCGCATA AGGCTAATGC GACTAGAAAA TTGATGAAAT GCATCGTGCC TTTTAAAGAC      180
AAAGAAGGGT ATGAGAGCCA AATCATTTTT TTAGACACTC CAGGGCTCCA TCATCAAGAA      240
AAATTACTCA ACCAGTGCAT GCTCTCACAG GCTTTAAAAG CGATGGGCGA TGCTGAATTG      300
CGCGTTTTTT TGGCTTCTGT GCATGATGAT TTGAAAGGGT ATGAAGAGTT TTTGAGTTTG      360
TGCCAAAAAC CCCATATCTT GGCTTTGAGT AAGATTGACA CAGCCACGCA TAAGCAGGTT      420
TTACAAAAAT TACAAGAGTA TCAAAAATAT TCATCGCAAT TTTTAGCTCT AGTGCCTTTG      480
AGTGCGAAAA AATCTCAAAA TTTAAACGCG CTTTTAGAAT GCATCAGTAA GCATTTAAGC      540
CCTAGCGCAT GGCTTTTTGA AAAGGATTTG ATGAGCGATG AAAAAATGCG CGATATTTAT      600
AAGGAAATCA TTAGGGAGAG TTTGTTTGAT TTTTGAGCG ATGAAATCCC TTATGAAAGC      660
GATGTGATGA TTGATAAATT TATAGAAGAA GAACGCATAG ACAAGGTGTA TGC GCGCATT      720
ATCGTAGAAA AAGAAAGCCA AAAAAAATC GTGATAGGTA AAAACGGGGT GAATATCAAA      780
CGCATCGGGA CTAACGCGCG ATTGAAAATG CAAGAAGTGG GCGAAAAAAA GGTTTTTTTA      840
AACTTGCAAG TGATCGCTCA AAAATCATGG AGTAAGGAAG AAAAAAGCTT GCAAAAAC TA      900
GGCTATATCT ATCAAAGGAA TAGGGAT      927

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(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116

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TTTCTGTCTC TAAGTCTCAT AGAAAGGGAC TTGAAACTA TGGCAAAGAT ATTAAACCT      60
AATTTAGATA GAGATGAGTT AAACACACTT TATAAGGCAA ATCTTGCTTA TGCTAAAAAC      120
ACGCATGAGC ATTATTTCAA ATTTAAAAAA GATGTAGACT ACAAACCTCT TAATCCTAGC      180
ATTATGCA TGCAATGTTT TATAAGCTTT GTAGCGGAC AAGGAGCTAA AAGATTATTA      240

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SUBSTITUTE SHEET (RULE 26)

811

TACATACTCT	ACAAGCTCGC	ATTTAATGCT	AAGTCTAATA	AGATTGCCCT	AGATAGACAT	300
TACGCCAAAA	TGTTTTTGCA	AGTTGTAGCA	AGAACTCTAA	TAAAGAATGT	CAATATATTA	360
GAAGAGCAAG	GTTTTATGTA	AGTCATTAAA	GGAAAACAAA	GATACTTGTA	TGTGTATCTT	420
AAAGATTACA	GAGAATTAGA	ATGCTTAGTG	AAGAGCAAGA	TGGCTAAGTA	TGTGATGTAT	480
TTAAGACAAT	TCTTTGATTA	TTGGATAGA	AAAAGGCGTT	ATGGCTTTGA	TTTTACGCTT	540
AAAAACCTAG	CCTTTGCTAA	GACCAAAGAA	AGCTTACCCA	GACATTTAAA	CGATAAAGAC	600
TTAAAGAGTT	TTTTAAAAAC	ACTCTTAGAC	TATAAGCCAG	CTACAAGCTT	TGAAAAACGC	660
AATAAGTGTA	TTCTACTTAT	TGTAATACTT	GGGGGACTTA	GAAAATGCGA	AGTGTAAAC	720
ATAGAATTAA	AACACATTCA	AGTAGAAGAG	CAAACTACT	CTATTTTAAT	TCAAGGTAAA	780
GGTAGAAAAG	AGAGAAAAGC	TTATATTAAA	AAGAGTTTGT	TAGAACCAAG	CTTGAATGCT	840
TGGATTAGTG	ATGATTACAG	ACTAAAATAT	TTCAATGGAG	CATATCTCTT	TAAAAAGGAT	900
AAGCAAAAAT	CACAAAATTC	TTTAACGCTT	TATAATTTTA	TCCCCTTAAT	CTTTAAATTA	960
GCCCAAATCA	AACATTACAA	ACAATATGGC	ACAGGCTTAC	ATCTATTTAG	GCATAGTTTT	1020
GCAACACTCA	TTTATCAAGA	AACCCAAGAC	TTAGTTTTAA	CTTCAAGGGC	GTTAGGGCAT	1080
AGCTCCTTAC	TCTCTACTAA	GATTTATATT	CATACCACAC	AAGAGCATAA	CAAGAAAGTG	1140
GCTCTTGTGT	TTGATAGTTT	GATAGAGAAC	AAGAAG			1176

(2) INFORMATION FOR SEQ ID NO:1117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117

AAAAGAAAGG	AACATTGCAT	GAAAAATTTA	AGGCATTTTA	GAAAGCTTAT	CGCCTTTTTA	60
GGTTTTTCAC	CTCTTTTATT	ACAAGCGGAT	ATGACTACCT	TTTTTAATTC	CATTGAACAA	120
CAGCTCACTA	GCCCTACGGC	TAAAGGCATT	TTAATGGTTA	TTTTTTTAGG	ACTTGCTATT	180
TTTATATGGA	AAAACTTAGA	TAGATGGAAA	GAAATTTTAA	TGACCGTGCT	TGCTTTAAAA	240
GAAGTCCCCA	TGCAATTAGT	TGCTATTTCA	GTTTCTAATC	TCAAAGAAAT	CAGCTCCAAA	300
GAAAAATTTT	TTTGGCTCAA	TGCTAAGAGT	TTTTTACTCT	CAGGATTTGT	GCCTTTTATT	360
ATGATACCTT	GGCTAGATAT	ATTGAACCTT	TTTGTGCTTT	ATGTGTGCTT	TCTCTTAATT	420
TTTAGCATAG	CGGAGTTCTT	TGATGAAGAT	ATAAGTGACA	TTTTAATCGC	TCATTCCAAA	480
ATTAAACCA	AAGCTAATTC	ATTTTACGCT				510

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

812

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118

AAGTCTCGCA	ACTTTAGCTA	TAATCAAACA	GAAGAAATTT	GGGAAACCA	CTTTAACTTA	60
TTTTCACTAG	GAATAGGCAT	GGCAGAAGAA	CAAGAAAATA	CCGCGCAACA	ACCCCAAAAA	120
AAAAGCAAAG	CCCTTTTATT	TGTCATTATT	GGAAGCGTGC	TAGTGATGCT	TTTATTGGTG	180
GGGGTGATTA	TCATGCTGCT	TATGGGGAAT	AAGGAAGAAT	CTAAAGAAAA	CGCTTCTAAA	240
AACACCCAAG	AAGTCCAAGC	TAATCCTATG	GCGAACAAGA	ATCAAGAAGC	CAAAGAAGGC	300
TCTAATATCC	AGCAATATTT	GGTGCTTGGG	CCTTTGTATG	CGATTGATGC	GCCTTTTGCG	360
GTGAATTTGG	TCTCTCAAAA	TGGCAGACGC	TACCTTAAGG	CTTCTATTTT	GCTAGAATTG	420
AGCAATGAAA	AGCTTTTGAA	TGAAGTCAAG	GTTAAAGACA	CGGCGATTAA	GGACACGATT	480
ATAGAAATTC	TATCGTCTAA	AAGCGTGGAA	GAAGTGTTTA	CTAACAAAGG	CAAAAACAAG	540
CTTAAAGATG	AAATTAGAG	CCATTGAAT	TCGTTTTTGA	TTGATGGCTT	TATTAAAAAT	600
GTCTTTTTCA	CTGATTTTCAT	TATCCAA				627

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119

GGAAGCATGA	TGACGGAAAT	GGAATTAAAG	CTCATTAAAA	TAGACACAAG	CCATTATTTT	60
GAAGAAAAAC	CAGGCTTGGG	GGAGAGAATG	GATTATGCGG	GTCGTTGTTA	TTATAATAAA	120
TTCCAAAGAG	TGAATGCCAT	GCTCACAAAG	TCGCTCATT	AAAAGCATT	GAAAAGGGAG	180
ATAGAAATCG	CGCACAACT	CATTTTGCCT	AACGATAAGG	TGGAAAACAT	CGTGTTTGAT	240
TATAATGGGA	GGAATCCGGA	GCGTTTTTAT	CATAAGGCGC	AGTTATTGCT	TCGTGAGGAA	300
GGTTTTATGA	ATTTTACCGC	TTATAACACG	AAGACGCCAG	GGCATTGCA	TTTGATATGT	360
CATAAGGGGC	ATACGGAATT	AGGCGAGGGT	GAAAGGCTGA	TTAAACTTT	ATCCATGAAA	420
TTAGCGCAAG	GGTTGCCTAA	AGAATGGAGG	GTTTTCCCTA	GCAATGAATG	GCCTAAGGAA	480
TTTAATATTT	TAGCTTTACC	TTATGAAGTG	TTTGCAAAAG	AGCGCGGGAG	CTCTTGGGCG	540
AAGCATTTA						549

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120

CCATTTTGA	AAGGATTTT	GATGTCAGAA	AAAGAAAGAC	TGAATGAAGT	GATCTTAGAA	60
GAAGAGAATA	ATGGGAGTGG	TACTAAAAAG	GTGTTTTTGA	TCGTGGCCAT	AGCCATTATC	120
ATTTTGGCGG	TGCTTTTAAT	GGTGTTTTGG	AAAAGCACCA	GAGTCGCTCC	TAAAGAGACT	180
TTTTTACAAA	CCGATAGTGG	CATGCAAAAA	ATAGGCAACA	CTAAAGATGA	GAAAAAAGAC	240
GATGAGTTTG	AAAGCTTGAA	TATGGATTCT	CCCAACAAG	AAGACAAGTT	AGACAAAGTG	300
GTGGATAATA	TTAAAAAACA	AGAGAGTGAA	AATTCTATGC	CCATTCAAAC	CGATCAAGCT	360
CAATGGAGA	TGAAAACAAC	AGAAGAAAAA	CAAGAATCTC	AAAAAGAATT	AAAAGCTGTT	420
GAGCCTATTC	CCATGAGCAC	TCAAAAAGAA	TCTCAGGCTG	TGGCTAAAAA	AGAAACCCCC	480
CATAAAAGC	CTAAAGTAGC	GCCAAAAGAT	AAAGAAGCGC	ATAAAGATAA	AGCTAAGCAT	540
GCAGCTAAAG	AGCCAAAAGT	CAAAAAGAA	GCTCGTAAAG	AAGTTTCTAA	GAAAGCTAAT	600
TCTAAACCA	ATCTTACTAA	AGGGCATTAT	TTGCAAGTGG	GGGTTTTTGC	GCACACGCCC	660
AACAAAGCCT	TTTTACAAGA	GTTTAATCAA	TTCCCCATA	AAATTGAAGA	TAGGGGGGCT	720
ACTAAACGCT	ACCTCATAGG	CCCTTATAAG	AGCAAGCAAG	AAGCCTTAAT	GCATGCCGAT	780
GAAGTCAGCA	AGAAGATGAC	TAAACCGGTT	GT CATAGAAG	TGCGG		825

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121

TCAAGGCTTC	AAAAAGCCAT	AATTAAGA	GTGAGATGT	TGGAAAACT	GATTGAAAGA	60
GTGTTGTTTG	CCACTCGTTG	GTTGCTAGCC	CCTTTATGCA	TTGCCATGTC	GTTAGTGTG	120
GTGGTTTTAG	GCTATGTGTT	CATGAAAGAG	TGTGGCACA	TGCTCAGCCA	TTTAGACACC	180
ATTAGTGA	CGGATTTGGT	TTTATCAGCC	TTAGGTTTAG	TGGATTTGTT	GTTTCATGGC	240
GGGCTTGTTT	TGATGGTGCT	GCTCGCCAGT	TATGAAAGCT	TGTTTTCTAA	ATTAGACAAG	300
GTGGATGCTA	GCGAAATCAC	TTGGCTAAAA	CACACAGATT	TTAACGCTTT	AAAATTAAAG	360
GTTTCCCTCT	CCATGTAGC	CATTTCCGCG	ATTTTCTTGC	TCAAACGCTA	CATGAGTTTA	420
GAAGACGTTT	TATCCAGTAT	TCCTAAAGAC	ACGCCCTAT	CGCATAACCC	TATTTTTTGG	480
CAAGTGGTGA	TCCATTTGGT	GTTTGTGTGT	TCAGCGCTGT	TAACCGCTGT	TACCAATAAC	540
ATCGCTTTTT	CGCAGAAAGA	AAGGCAT				567

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122

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GGTTTGAAC ATATTGATT GCGTTACTT GTGCTAGTGG TAGCCTTTGG GATTAGGGGG      60
TTTTATCATG GCTTCGTGAG TGAAATAGCA GCGACTTTGG GGATTGTGCT TGGCGTTTAT      120
TTGGCGTCTC GCTATTCTGT GGCTGTTGGG AATTATTATT CAGAGCATTT GTATGATTTA      180
AGAAATGAAA CCATGACCAA TCTCATTGGT TTTTACTTGG TGTGGCGTC CATTGGGGTG      240
TTTTTTTAG CTCTTGAGT GTTGCTAGGC AAGATGTTAG TCTTTAGCGG TCTAGGCATT      300
ATAGACAAGG CGTTAGGGTT TATTTTTTCA TGTTTGAAGA CTTTTTAGT GCTTCTTTC      360
ATCCTTTATG CGCTCTCTAA AATGGATTTA ATGAAAGACG CTAACGCCTA TTTGCAAGAA      420
AAGAGCGCTA TTTTCCCCAC CATGAAAAGC GTCGCTAGTA AGATCATGCG CCTTGATGGC      480
GTCAACATG TGAGAAAAA CCTTAAAGAC AACCTTGAAG AAATGAGCGA TGAAGTTAAA      540
AATAAAGGAT CTATTGATAA CGCCAAAGAA TCTTTTAATA AGGCTACGGA TAAGGGCGTA      600
GAAGCTTTAA AAGAAAAGGC TAAAGATTG CTAATAAACA TGCTAGAGCC AAAACACAAT      660
AAACCAACC AAACCCACC AATCCAACC CCATCTAATA AAGAACCCT A              711

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(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123

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AGCTTATGGG TTGAAAACCC TATATTACTA TCACACTCAC AAGTCTATAG CCCCCAAGA      60
TGCTGGGTTT TTAACCCCT TAGAAACAGC GCTTTTGCTT TGGGTTTTTT CGTGGGGGCG      120
TTATTGTTTT ACTGGTGCGC TTTAAGGCTT TCGCATTCCG ATTTCACTTA TTTATTGCCC      180

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SUBSTITUTE SHEET (RULE 26)

815

TTAATCATTG	TTTGTAGTAGC	GTTAGTTTTAT	GGGGTTTTTAT	TTTATTTGTT	GCTCTATTTT	240
GAAAACCCCT	ACTTCAGGCT	TTTGAGTTTTT	TTAGGCTCTA	GTTTTATCCA	CCCTTTTGGA	300
TTTGATTGGT	TAGTCCCGGA	TAGCTTTTTT	TCTTATAGCG	TGTTTAGGGT	GGATAAATTA	360
TCTTTAGGGC	TTATTTTTTT	AGCTTGCATT	TTTTTGAGCG	CTCAAAATCT	TAAAAAATAC	420
AGAATGATAG	GGGTTTTATT	GCTGCTTGGC	GCGTTGGATT	TTCATTTTTT	TAAAAATAAGC	480
GATTTAAAAG	AGGTTGGAAA	TATTGAATTA	GTCTCTACAA	GAACGCCCCA	AGATTTGAAA	540
TTTGACTCAA	ATTACCTTAA	TAATATTGAA	AACAACATT	TTAAAGAAAT	CAAACCTCGCT	600
CAAAGCAAGC	AAAAAACCTT	GATTGTTTTT	CCAGAGACCG	CTTACCCTAT	CGCTTTAGAA	660
AACTCCCTT	TTAAAACCCA	ACTAGAAGAT	TTAAGCGCCA	AGATCGCCAT	TTTAATAGGG	720
ACATTGCGCG	CTCAAGGCTA	TAGCCTTTAT	AACAGCTCGT	TTTTATTTTC	TAAAAAAAAGC	780
GTTCAAATCG	CTGATAAAGT	GATCTTAGCC	CCCTTTGGCG	AGATAATGCC	TTTACCGGAG	840
TTTCTTCAAA	AACCCCTTGA	AAAGCTCTTT	TTTGGCGAGA	GCGCTTATTT	ATACCGCAAC	900
GCTCCCCATT	TCAGCGATT	TACATTAGAC	GATTTCACCT	TTGCGCCCTT	GATTTGCTAT	960
GAAGGCACTT	CCAAACCCGC	TTATTCAAGC	AGCCCTTCAA	AAGTTTTTAT	CCTAATGAGC	1020
AATAACGCAT	GGTTTAGCCC	AAGCATTGAA	CCCACCTTAC	AAAGAACGCT	TTTAAATAC	1080
TACGCAAGGC	GTTATGATAA	AATCATCTTG	CACAGCGCGA	ACTTTTCAAC	TTCTTACATT	1140
TTAAGCCCTA	GCTTATTGGG	CGATATTCTT	TTTAGGAAAC	GATCA		1185

(2) INFORMATION FOR SEQ ID NO:1124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124

GAAACGATCA	TGATTAAAGC	GATTGATATT	TCTCATGCTT	TTGAAAAACC	TCTTTATAAT	60
GGCGTGAATT	TGCGCATTA	ACCCAAAGAA	AGCCTGGCGA	TTTAGGCGT	GAGCGGGAGC	120
GGTAAAAGCA	CGCTTTTAA	CCATTGCGC	ACCATGCTAA	AACCGGATAG	CGGAACAGTC	180
AGTTTGTTAG	AACACCAAGA	TATTATGCC	CTAAATTCCA	AAAAGCTTTT	GGAATTGCGG	240
CGCTTAAAAG	TGGGCATCGT	TTTTCAATCG	CATTACCTTT	TTAAGGTTT	TAGCGCTTTA	300
GAAAACTTGC	AAGTCGCTTC	AATCCTAGCC	AAGCAAGAAA	TAAATCATTC	CCTTTTAGAA	360
CAATTAGGCA	TAGCCACAC	CCTAAAACAA	GGCGTGGGCG	AATTGAGCGG	CGGCCAGCAA	420
CAACGCTTAA	GCATCGCCAG	AGTGCTTTCT	AAAAAACCCC	AAATCATTAT	CGTGATGAA	480
CCCACCGGGA	ATTTAGACAC	CACTAGCGCT	AATCAAGTCA	TCAGCATGCT	GCAAAATTAC	540
ATTACAGAAA	ACGAAGGGC	GTTAGTCTTA	GCCACGCATG	ATGAGCATTT	AGCCTTCACT	600
TGCTCTCAAG	TCTATCGCCT	AGAAAAAGAA	TCTTTGATTA	AGGAAAAA		648

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

816

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125

TCGCTCGCCC CTAAATTAAA AGCGTTTTTT AAGGTAGCGT TATCCTGTAA GGCGGTGATA	60
AAAATCACAG GCGTAGAGAT TAAAAAATCG TTTTGTATGC GCTTGAATAA TTCCAAGCTA	120
TTCAATTCAG GCACTTGACG GTCTAAAAGC AAGAGGTAA AGCGCTCAAC AGAGAGCCTT	180
TCA	183

(2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...900
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126

TTTGCGTTGC ATAAAAAGT TCTGTTGGCT TTAAGTCCCA GCTTGATTG CCAAGAGTCT	60
TTGTTGCGCTA AGGATAAAGA CTACACTTTG GGCAAGGTTT CTACTGCCGG TAAAAAGGAT	120
AGATCTGACT ATCTCGGGCA GGTCAATTTG GGTATAGCG GGATTACCGC GCCTAAGAGT	180
TGGCAAGATG AAGAAGTGAA AAAATACACA GGAAGCCGCA CGGTGATCTC TAACAAAGCG	240
CTCACCCAAC AAGCTAACCA AAGCATTGAA GAAGCTTTAC AGAATGTCCC CGGTCTGCAA	300
ATTAGGAATG CCACAGGTGT GGGGGCTATG CCTACTATCC AAATCCGTGG CTTTGGAGCG	360
GGGGGTTTCA GGCATAGCGA TCGACGCTC ATGTTAGTTA ATGGTATTCC TGTATTATG	420
GCCCCTTACG CTCACATTGA GCTAGACATT TTCCCTGTTA CCTTTCAAGC CATTGATCGC	480
ATTGATGTGA TCAAAGGTGG AGGCAGCGTG CAATATGGGC CTAACACTTA TGGGGGTATT	540
GTCAATATCA TCACTAAACC TATCCCTAAT CAATGGGAAA ACCAAGCGGC TGAAAGGATC	600
ACTTATTGGG CTAAGGCTAG AAACGCTGGG TTTGCCGCTC CCCCTGATAA AACCGGCGAT	660
CCTTCTTTCA TCAAGTCTTT AGGCAACAAC CTCCTCTATA AACTTATGT GAGGAGCGGA	720
GGGATGATCA ATAAGCATGT GGGTATCCAA GCGCAAGCTA ACTGGGTTAG AGGCCAAGGC	780
TTTAGGGACA ATAGCCCCTC TAGTATTTC AACTATTGGC TGGATGGGGT CTATGACATC	840
AATGAAAGCA ATGGGATTAA AGCCTATTAC CAATACTACG ATTTTGCTAT CGCCCAACCG	900

(2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

817

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127

GTGTCAATAC	TAGTTATAAT	AGAACCTTAC	ACTTTTTTACA	AAAGGGAGGA	GAGTGTCATG	60
TTGGGGAGCG	TCAAAAAAGC	GGTTTTTAGG	GTTTTGTGTT	TGGGGGCGTT	GTGTTTATGC	120
GGGGGGTTAA	TGGCAGAGCA	AGATCCTAAA	GAGCTTATAT	TTTCAGGTAT	AACTATTTAC	180
ACGGATAAAA	ATTTCACTAG	AGCTAAGAAA	TATTTTGAAA	AAGCTTGCAA	ATCAAACGAT	240
GCTGATGGCT	GTGCAATCTT	AAGAGAGGTT	TATTCTAGTG	GTAAAGCCAT	AGCGAGAGAA	300
AACGCAAGAG	AGAGCATTGA	AAAAGCTCTT	GAACACACCG	CTACTGCTAA	AGTTTGTAAG	360
TTAAACGATG	CTGAAAAATG	CAAGGACTTA	GCAGAGTTTT	ATTTTAATGT	AAACGATCTT	420
AAAAATGCTT	TAGAAATATTA	CTCTAAATCT	TGTAAGTTAA	ATAATGTTGA	AGGGTGATG	480
CTGTCAGCAA	CTTTTATATA	CGATATGATA	AAGGGTTTGA	AAAAAGATAA	AAAAGATCTA	540
GAATATTATT	CTAAAGCTTG	CGAGTTAAAT	AACGGTGGAG	GGTGTTCTAA	ATTAGGAGGG	600
GATTATTTTT	TTGGTGAAGG	CGTAACAAAA	GATTTCAAAA	AAGCTTTTGA	ATATTCTGCC	660
AAAGCTTGCG	AGTTGAACGA	TGCTAAAGGG	TGTTACGCTC	TAGCAGCGTT	TTATAATGAG	720
GGTAAAGGCG	TGGCAAAGGA	TGAAAAGCAA	ACGACAGAAA	ACCTTGAAAA	GAGTTGCAAG	780
CTAGGATTAA	AAGAAGCATG	CGATATTCTC	AAAGAACAAA	AACAA		825

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128

ACCCGCAAAAT	CATCAGCATC	CATGTCAGAA	AATGAAAAAC	ACCCCATAG	GGTGTTGCAA	60
CTCATTAATA	GTTCAAGCAT	CACGCCAGGC	ATTGTCCTAA	ACCCCCACAC	GCATGAAGAA	120
AGTATTAAAT	ACTTGCTAGA	AAGCGTGGGG	CTAGTGCTTT	TAATGAGCGT	GAATCCGGGC	180
TTTGCGGGGC	AGAAGTTTTT	AGATCTAGTG	CTAGAAAAAGT	GCTTGAAAGT	TAAAGAACTG	240
ATCAAACGCT	ACAACCTAG	CTGCTCTTTA	GAAGTGGATG	GGGGCGTGAA	TGATAAAAAAT	300
ATCTTTGAAC	TCCAACAAGC	GGGCGTGGAT	GTGGTGGTTT	CAGGGAGTTA	TATTTTGA	360
TCCAAGATC	GTAAGCTGGC	TATTGAAGGC	TTACAGAATG	TCAGACAACC	TCTTGCA	417

SUBSTITUTE SHEET (RULE 26)

818

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129

AAACTTTTAA	GAGTTTTACA	TAAGATGATT	AAAAAAGCGG	CTAAAACCCC	TTTTTTTAAA	60
ATTTTGTTC	AAGCTTTAAG	CTACAATATA	CGCATGAAAG	ATTTAAACAA	GACTATCGGC	120
GTGTTTGTGC	GGCCCACTCA	TCATCAAAAC	GCTCTTTTTA	AAGAGCTAGA	GCAGGCTAAA	180
GAATGGGTTT	TAACGCTTTT	AGAAGATGAG	GGGTTTGAAA	GCTTTATGAT	TGATAGCCTT	240
GATGGGGCAA	AAGATGCACA	ATTGATAAAA	AAAGCTTACG	CGTTTTTGTG	TTTAGGAGGC	300
GATGGCACGA	TTTAGGGGCG	TTTAAGAATG	ACGCATGCTC	ACAATAAGCC	ATGCTTTGGG	360
GTGAGGATTG	GGAAATTTAGG	GTTTTTGAGC	GCGGTIGAAT	TGAACGGGTT	GAAAGATTTC	420
TTACAAGATC	TCAAGCAAAA	CAGGATCAAA	TTAGAAGAGC	ATTTGGCTTT	GGAGGGCCGT	480
ATTGGAAACA	CTTCTTTTTA	TGCGATCAAT	GAAATCGTGA	TCGCTAAAAA	AAAAGCTTTA	540
GGGGTTTTAG	ACATCAAAGC	GTGCGCGGGC	CATACGCCCT	TTAACTTA	TAAAGGCGAT	600
GGGCTTATGC	TTGCCACGCC	CCTAGGCTCA	ACCGCTTATA	ATTTGAGCGC	TCATGGGCCC	660
ATTGTGCATG	CTTTAAGCCA	AAGCTATATT	TTAACGCCCT	TGTGCGATTT	TTCTTTAACG	720
CAACGCCCTT	TAGTGTTAGG	GGCGGAATTT	TGCTTGAGTT	TTTGCGCTCA	TGAAGACGCT	780
CTTGTTGGTTA	TTGATGGGCA	AGCCACCTAC	GATTTAAAAG	CCAACCAACC	CCTATACATT	840
CAAAAAGGCC	CCACGACCAC	CAAGCTCTTA	CAAAAAAATT	CAAGGGATTA	TTTTAAAGTG	900
CTTAAAGAAA	AGCTGTTATG	GGGGGAAAGC	CCTAACAAAA	AAAGA		945

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130

CGCTACAATA	CCCCCATGCA	AAAAAAGATT	TTTTTACTAG	AAGACGATTA	CCTTTTAAGC	60
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SUBSTITUTE SHEET (RULE 26)

819

GAGAGTATCA	AGGAGTTCTT	GGAGCATTTA	GGCTATGAAG	TGTTTTGCGC	TTTTAACGGG	120
AAAGAGGGCT	ATGAAAGGCT	CTCTGTTGAG	CGCTTTAACC	TCTTGCTTTT	AGACGTGCAA	180
GTGCCTGAAA	TGAATAGCTT	GGAATTATTC	AAGCGCATCA	AAAACGATTT	TTTAATCTCT	240
ACGCCTGTGA	TTTTTATCAC	CGCCTTACAG	GATAACGCTA	CCTTAAAAAA	CGCTTTTAAT	300
TTAGGGGCGA	GCGATTATTT	GAAAAAGCCT	TTTGATTGGG	ACGAATTGGA	AGCGCGCATT	360
AAAAGGTTTT	TCAATGATGA	TCCGATAGAA	ATCATGCCTA	ACATTTTTTA	CCACCAACAC	420
GCTTTGAACG	TTAAAGGGAA	AAAGGAAATC	TTAGCGCCCA	AAACCGCCCA	ACTTTTAGAA	480
TATTTTTTAG	AGCATAAAGG	GCAAATCATC	AGCTCTCAAG	CGTTAGAAAA	CAACTTATGG	540
GAGCAAGCGA	TTGATGATTC	CACCTTACGC	ACTTACATTA	AAGTGTTCGC	CAAGCTTTTG	600
GGTAAAAATT	GCATAGAAAC	GCATAAGGGG	GTGGGCTATC	GCTTTAACCC	ACTA	654

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131

TGTGGCGCTA	ATCGCTCAAA	AGGGCGTGGA	GGTTTTAGTT	CAAAATGCGC	GGGCGCGAAT	60
AGCGGTTATA	GTAACGAAGC	GTATGAAAGC	GTGGGGGCTA	AAATCGTGGA	TTCTAAACG	120
GCGTGGGGGC	AGGATTGGT	GGTCAAATGC	AAAGAGCCTT	TAGAGCATGA	ATACCCCTTG	180
CTCAAAGAAA	AAGCGACTCT	GTTTAGTTAT	TTGGATTTAG	CGTATCAAAA	AAGCTTGTGT	240
GAAATGTTTA	TTAATAAAAA	AATCACTTCT	ATTTGCACTG	AAACCATTGC	CGGGCCATAA	300
AACGACTACC	CTATTTTAGC	GCCTATGAGC	GTGGTGGCTG	GGAGGTGGC	TGCGCATTTA	360
GTCCAGCATT	ATTTACTGGC	TTTAGAGCAT	GTTAAAGGGT	TTATGGGTAA	GGGGGTCATG	420
CTAGGGGGTT	TGTCGGGTGC	GCAAAGGGCT	AAAATCGTCG	TAATTGGAGG	CGGTGTGGTT	480
GGCATGGAGA	GCGCGAAAGT	CCTAAGCCAA	ATGGGGGCTA	AAGTAACGAT	TTTAGAATTA	540
GACTACGCTA	AATTACAAAA	CCACCCCTAT	TATCATTGTG	ATGATTTAGA	AGTCTTAAGC	600
GTGAATGAAG	CCAATATCAT	TCAAGCCTTA	AACGGGGCGG	TGGGGCTAGT	GGGAGCGGTG	660
CTGGTTACAG	CGAGCCAAAC	CCCTAAAGTG	ATCTTAAGAA	GGCATTAAAA	ATACATGCAG	720
ACACAAGGGG	TAGTCATTGA	TGTGGCTTGC	AGTTTAGGGG	GGTGCATAAG	AGCCATACGC	780
CAAGCAAGCC	ATTCTAACCC	GGTGTATGTG	GAAGAAAGTT	TGTTCATTAA	TGGCGTGCCG	840
AACATGCCAG	GGATTGTTCG	TAAACGAGC	TCTACGGCTT	ATAGCCATGC	GAGTGTGCCG	900
TATTTGTTGT	ATTATTTAGA	GCATGGCTTG	AAGGGTTTTT	TAACAGCCAA	CACTAAAATC	960
GTGGCGAACA	CGCTTGAGG	CTTGAGCGCT	TATAACGGCT	ATATCACCCA	AGAAGGCATC	1020
GCTAAAGCGT	TCAATCTGGC	GTTCAAATCG	CCTTTAGAAA	TTTTAAAGGA	GCTT	1074

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

820

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132

AAGGGTAAAA	GGGTAAAAAA	CATGCGAGAT	TTCAATAACA	TTCAAATCAC	ACGCTTAAAA	60
GTGCGTCAAA	ATGCCGTTTT	TGAAAAACTG	GATCTGGAGT	TTAAAGATGG	CTTGAGCGCG	120
ATTAGTGGGG	CTAGTGGGGT	GGGGAAGC	GTCTTATTG	CGAGCCTTTT	AGGGGCGTTT	180
GGGCTTAAAG	AGAGCAACGC	TTCAAACATT	GAAGTGAAT	TGATCGCGCC	TTTTTTAGAC	240
ACGGAAGAAT	ACGGCATT	TAGAGAAGAT	GAGCATGAAC	CCTTAGTTAT	TAGCGTGATT	300
AAAAAAGAAA	AAACACGCTA	TTTTTTAAAC	CAAACAAGCC	TATCTAAAAA	CACGCTCAAA	360
GCGTTATTAA	AGGGGCTTAT	TAAACGCTTA	TCTAACGACA	GATTCAGCCA	GAATGAACTC	420
AACGATATTT	TAATGCTCTC	CTTATTAGAT	GGCTATATCC	AAAATAAAAA	TAGGCGTTTA	480
CCCCCCTTT						489

(2) INFORMATION FOR SEQ ID NO:1133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 891 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133

TCAAATCATA	AAAGGGTTTT	TATGGATTAC	AAACGTTTTA	AAGGCAAGCA	TGCGAACATC	60
GTTATAGAAA	TCATCAGTCT	TTTAGAAAAA	GGGGTTAAAA	AAGCCCAAGA	GATTTTAGAA	120
AAGCCGGACG	CTGGGAGTTA	CACTCAGTTA	GAAAACAGCA	GCGGGGATAC	GCCTATTAAA	180
GCGGATTTAG	CCCTAGATAA	GTTTTTAGAG	GAAACTTTTT	TGAGTTTAGA	GAATGTGAAA	240
AGCGTTTTTA	GCGAAGAAAA	AGAAACGCCT	GTTACTAAAG	AAAACGGCTC	TTATTTGATC	300
GCTTATGACC	CCCTAGATGG	GAGTTCAGTG	ATGGAGGCGA	ATTTCTTAGT	AGGCACGATT	360
ATAGGGGTTT	ATGAAAAGGA	TTATAAGGCG	CAAAATTTAG	TTGCAAGCCT	TTATGTGGTT	420
TTTGGGCATA	AAATAGAATT	GGTGGTGGCT	TTAGAAGAAG	TTATCGTTA	CGCTTTTAT	480
CAAAACAAGT	TTCATTTTAT	AGAAACCATC	GTTTTAGAAA	ATAAGGGTAA	AATCATCGCT	540
AGCGGAGGCA	ATCAAAAGGA	TTTTTCTTTG	GGCTTAAAAA	AGGCTTTAGA	AGGGTTTTTT	600
GCAGAAAATT	ACCGCTTGCG	ATACTCAGGA	TCTATGGTGG	CTGATGTCCA	TCATGTGTTG	660
GTTAAAAAGG	GCGGAATGTT	TTCCTACCCG	CAAAAGAAAT	TGCGAAAGCT	TTTTGAAGTC	720
TTTCCTTTAG	CCTTGATGGT	TGAAAAGCT	AAAGGGGAAG	CGTTTTATTT	TGATAAGGGG	780
GTTAAAAAGC	GTTTGCTAGA	TCAAAGCGTA	GAAAGCTACC	ATGAAAAAAG	CGAATGCTAT	840
TTAGCCAGCC	CGCATGAAGC	TCAGATTTTA	GAAAACATT	TAAAGGGAGA	A	891

(2) INFORMATION FOR SEQ ID NO:1134:

SUBSTITUTE SHEET (RULE 26)

821

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134

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ACTTTTTTAA TTATTTTTTG GGTATTCTTT TTAAGAATTA AGCATTATGT TAAGGAATTA      60
TCCATGAAAA AATTTTTTTC TCAATCTTTG TTAGCTCTTA TTATCTCTAT GAATGCGGTA      120
TCTGGCATGG ATGTAATGG CGTTTTTTA GGGGCGGGTT ATTGCAAGG ACAGGCGCAA      180
ATGCATGCGG ATATTAATTC TCAAAAACAA GCCACCAACG CTACGATCAA AGGCTTTGAC      240
GCGCTCTTGG GGTATCAATT TTCTTTTGAA AAACACTTTG GCTTACGCCT TTATGGGTTT      300
TTTGACTACG CTCATGCCAA TTCTATTAAG CTTAAAAACC CTAATAATA TAGCGAAGCG      360
GCGCAAGTGG CTAGTCAAAT TCTTGGGAAA CAAGAAATCA ATCGTTTAAC AAACATTGCC      420
GATCCCAGAA CTTTTGAGCC GAACATGCTC ACTTATGGGG GGGCTATGGA CGTGATGGTT      480
AATGTCATCA ATAACGGCAT CATGAGTTTG GGGGCTTTTG GCGGGATACA ATTGGCCGGC      540
AATTCATGGC TTATGGCGAC ACCGAGCTTT GAGGGCATT TAGTGGAACA AGCCCTTGTC      600
AGCAAGAAAG CCACTTCTTT CCAATTTTTA TTCAATGTGG GGGCTCGCTT AAGGATCTTA      660
AAACATTCTA GCATTGAAGC GGGCGTGAAA TTCCCCATGC TAAAGAAAAA CCCCTACATC      720
ACTGCAAAAA ATTGGATAT AGGGTTTAGG CGCGTGATT CGTGGTATGT GAATTACGTG      780
TTCACTTTC

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(2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135

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TGGATTGACG CTAAAAATAA AGAAGAAGCC ATCATTCAAG GCTACACTAT CATTGATCCA      60
AGCACCGTTA TTGCCACGCA CACCAGCGAA TTAGTGAAAA AATACGCTGA AGATTTTATC      120
ACCAAAGATG AAGTGAAATC CCTTTTAGAG CGCTTGCGTA AAGACTATCC TACGATTGTA      180
GAAGAGAGTA AAAAAATCCC CACCGTGCG ATCCGCTCAG TCTTGCAAGC CTTGTTGCAT      240

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SUBSTITUTE SHEET (RULE 26)

822

GAAAAAATCC	CCATTAAGGA	CATGCTCACT	ATTTTGAAAA	CGATTACTGA	TATTGCTCCA	300
TTGGTTCAAA	ACGATGTGAA	TATCTTAACC	GAACAAGTGA	GGGCGAGGCT	TTCTAGGGTG	360
ATCACCAACG	CTTTTAAATC	TGAAGACGGG	CGTTTGAAAT	TTTTAACCTT	TTCTACCGAT	420
AGCGAACAAAT	TTTGCTCAA	TAAATTGCGA	GAAAAATGGCA	CCTCTAAGAG	CTTATTACTC	480
AATGTGGGCG	AATTGCAAAA	ACTCATTGAA	GGGGTTTCTG	AAGAGGCTAT	GAAAGCTTG	540
CAAAAAGGGA	TCGCTCCGGT	GATTTTGATT	GTAGAGCCTA	ATTTAAGAAA	AGCCCTTTCT	600
AATCAAATGG	AGCAGGCTAG	GATTGATGTG	GTCGTGCTAA	GCCATGCGGA	ATTAGATCCT	660
AACTCTAATT	TTGAAGCCTT	AGGCACGATC	CACATTAACT	TT		702

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136

AAAAAAAGA	CCCTAAACAT	TTCACAATTA	GGAAAAACCA	TGCATGTTGC	TTGTCTTTTG	60
GCTTTAGGGG	ATAACCTCAT	CACGCTTAGC	CTTTTAAAG	AAATCGCTTC	CAAACAGCAA	120
CAGTCCCTTA	AAATCCTAGG	CACTCATTG	ACTTTAAAA	TCGCCAAGCT	TTTAGAATGC	180
GAAAAACATT	TTGAAATCAT	TCCTGTTTTT	GAAAAATATCC	CTGCTTTTTA	TGACCTTAAA	240
AAACAAGGCG	TTTTTTGGGC	GATGAAGGAT	TTTTTATGGT	TATTAAGAGC	AATTAAAAAA	300
CATCAAAATCA	AACGTTTGAT	TTTAGAAAAA	CAAGATTTTA	GAAGTTTTCT	TTTATCCCAA	360
TTTGTTTCCA	TAACCACTCC	AAATAAGAA	ATTAAAAACG	TTTATCAAAA	CCGCCAGGAG	420
TTGTTTCTC	AAATTATGG	GCATGTTTTT	GATAACCCCTC	CATATCCCAT	GAGTTTAAAA	480
AACCCCAAAA	AGATTTTGAT	CAACCCCTTC	ACAAGAGAAA	ATGATAGGAA	TATTTCTTTA	540
GAGCATTTAA	AAATCGTTTT	AAAACCTCTA	AAACCCCTTT	GTGTTACGCT	TTTAGATTTT	600
GAAGAACGAT	ACGCTTTTTT	AAAAGACAGA	GTCGCTCATT	ATCGCGCTAA	AACCAGTTTA	660
GAAGAAGTTA	AAAACCTGAT	TTTAGAAAGC	GATTTGTATA	TAGGGGGGGA	TTCGTTTTTG	720
ATCCATTG	CTTACTATTT	AAAGAAAAAT	TATTTTATCT	TTTTTTATAG	GGATAATGAC	780
GATTTTCATG	CGCCTAATAG	TGGGAATGAG	AAATTCCTAA	AAGCCCATAA	AAGCCATTTT	840
ATAGAACAGG	ATTTAGCCAA	AAAATTCGCG	CATTTGGGGC	TATTA		885

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137

AACACACAGC	GCCAAACACT	CCCCCTAGTC	AAGTCCCGCC	CACACCCCTT	AGTCAAAATT	60
TACCTAAAAC	AAATGTGTGG	AATGGGGTTT	ATTGGCTTCA	AAACAAAAC	TACTCAAACA	120
AAGGCATTTA	TTATATTGAT	CCCAATCTTT	CAGGACAGAG	CGGTCAAAGC	GGCAACACGC	180
TCAGCACCTA	TACAGCTAAT	TTGT				204

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...4239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138

ACGCTAATAT	CAATTTTCAG	CGCAAGCCAG	GCTGATTTTG	GAGGCAACAC	GACTATTGAT	60
ACAGCAAGCT	TTAATTTTGA	CAGCGCAAGT	TCATTGAATT	TTAATAACCT	TACGGCTAAT	120
GGGGCGTTAA	ATTTTAAATGG	TTATGCGCCC	TCTTTAACTA	AGGCTTTAAT	GAATGTCAGC	180
GGGCAGTTTG	TTTATGGGAA	TAATGGGGAT	ATTAATTAT	CTGACATCAA	TATCTTTGAC	240
AACATCACAA	AATCTGTAA	TTACAACATC	TTAAACGCTC	AAAAAGGGAT	TACTGGCATT	300
AGTGGGGCTA	ATGGCTATGA	AAAAATCCTT	TTTATGGCA	TGAAAATCCA	AAACGCTACC	360
TATAGCGATA	ATAACAACAT	CCAAACTTGG	TCGTTTATAA	ACCCTCTCAA	TTCTTCTCAA	420
ATCATTCAAG	AGAGCATTA	AAATGGGGAT	CTAACCATAG	AAGTTTTTAA	TAACCCTAAC	480
TCGGCTTCCA	ACACTATTTT	TAATATCGCT	CCTGAGCTTT	ATAATTACCA	AGATTCTAAG	540
CAAAATCCTA	CCGGCTATAG	CTATGATTAT	AGCGACAATC	AAGCAGGCAC	TTATTACTTG	600
ACAAGCAACA	TTAAAGGTCT	TTTCACCCCT	AAAGGCTCTC	AAACGCCCTCA	AACCCCAAGC	660
ACTTATAGCC	CATTTAACCA	GCCTTTGAAT	AGTTTGAATA	TCTACAATAA	GGGTTTTTCT	720
AGCGAGAATT	TAAAAACGCT	TTTAGGGATC	CTTCTCTCAA	ATTCCGCCAC	CTTAAAAGAA	780
ATGATTGAAT	CCAACCAACT	AGACAATATC	ACTAACATTA	ATGAAGTGTT	GCAACTCTTA	840
GATAAGATTA	AAATCACCCA	AGCGCAAAAG	CAAGCGCTCC	TAGAAACGAT	CAACCATTTG	900
ACTGACAACA	TCAATCAAAC	CTTTAATAAC	GGGAATCTCG	TTATAGGCGC	TACCCAAGAT	960
AATGTTACAA	ACTCTACTAG	CTCTATATGG	TTTGGGGGCA	ATGGCTATAG	CAGCCCTTGC	1020
GGCTAGATA	GCGCCACTTG	TTCTTCTTTT	AGAAACACTT	ACTTGGGGCA	ATTATTAGGC	1080
TCAACTTCCC	CTTATTTAGG	CTACATTAAC	GCTGATTTTA	AAGCTAAAAG	CATTTATATT	1140
ACCGGGACAA	TTGGAAGTAG	TAACGCTTTT	GAAAGCGGAG	GGAGCGCGGA	TGTAACCTTT	1200
CAAAGCGCTA	ATAACTTAGT	GTTGAATAAA	GCTAACATAG	AAGCTCAAGC	CACAGACAAT	1260
ATCTTTAATC	TTTGGGTCA	AGAAGGGATT	GATAAAATCT	TTAATCAGGG	GAATTTAGCG	1320
AATGTTCTTA	GTCAAATGCG	TATGGAAAAA	ATCAAGCAAG	CCGGCGGTTT	AGGGAACTTT	1380
ATAGAAAACG	CTCTAAGCCC	TTTGAGTAAG	GAATTACCCG	CTAGCTTGCA	AGATGAAACC	1440
TTAGGCCAAC	TTATAGGTCA	AAATAACTTA	GATGATTAT	TGAATAATAG	TGGAGTCATG	1500
AATGAAATCC	AAAACATTAT	CAGTCAAAAA	CTAAGCATTT	TTGGCAATTT	TGTTACCCCA	1560
TCCATCATAG	AAAACACCT	TGCTAAGCAG	TCTTTAAAAA	GCATGCTAGA	CGATAAAGGG	1620
CTTTTGAATT	TTATCGGTGG	GTATATAGAC	GCTTCTGAAT	TAAGCTCTAT	TTTAGGCGTG	1680

824

ATTTTAAAGG	ATATTACTAA	CCCCCTACA	AGCCTGCAAA	AAGACATTGG	TGTGGTAGCG	1740
AACGACTTGT	TGAACGAGTT	TTTAGGACAA	GATGTTGTCA	AAAAGCTAGA	AAGTCAAGGC	1800
TTGGTGAGTA	ATATCATCAA	TAATGTTATT	TCTCAAGGCG	GGTTGAGCGG	CGTTTATAAT	1860
CAAGGTTTAG	GGAGCGTGTT	GCCGCCCTCT	TTACAAAACG	CGCTCAAAGA	AAACGATTTA	1920
GGCACTCTTT	TATCGCCTAG	AGGCTTGCAT	GATTTTTTGGC	AAAAAGGGTA	TTTTAACTTT	1980
TTAAGCAATG	GCTATGTTTT	TGTCAATAAC	AGCTCTTTTA	GTAACGCTAC	TGGGGGTAGT	2040
TTGAATTTTG	TGCGCAACAA	GTCTATTATC	TTTAATGGCG	ATAATACGAT	TGACTTTAGC	2100
AAGTATCAAG	GCGCATTGAT	TTTTGCTTCT	AATGGTGTIT	CTAATATCAA	TATCACCACC	2160
CTAAACGCCA	CTAATGGCTT	AAGCCTTAAT	GCGGGTTTGA	ATAATGTGAG	CGTTCAAAAA	2220
GGAGAAATTT	GTATCAATTT	AGCCAATTGC	CCTACAACCA	AAAACAGCTC	TCCTGCAAAC	2280
TCTAGCGTAA	CCCCCACTAA	TGAGTCTTTA	AGCGTGCACG	CTAATAATT	CACTTTCTTA	2340
GGCACAATCA	TCTCTAATGG	GGCTATTGAT	TTGTCTCAAG	TAACAAATAA	TAGCGTTATA	2400
GGCAGCTCA	ATCTCAATGA	AAATGCGACC	TTGCAAGCTA	ATAATTTAAC	GATCACCAC	2460
GCTTTTAACA	ACGCCCTCTA	CTCTACGGCT	AATATTGATG	GTAATTTTAC	CTTAAACCAA	2520
CAAGCGACTT	TAAGCACTAA	CGTAGTGGT	TTGAATGTCA	TGGGGAATTT	TAATAGCTAT	2580
GGCGATTGG	TGTTTAACCT	CAGTCATTCA	GTTAGTCATG	CTATTATCAA	TACTCAAGGC	2640
ACAGCGACGA	TCATGGCCAA	TAATAACCTT	TTGATCCAAT	TCAACGCTTC	TTCACCAGAA	2700
GTGGGTACTT	ACACGCTGAT	TGATAGCGCT	AAAGCCATT	ATTACGGGTA	TAACAACCAA	2760
ATCACAGGAG	GCGTAGCCT	GGATAATTAC	CTTAAGCTTT	ATGCGCTCAT	TGATATTAA	2820
GGCAAGCACA	TGGTGATGAC	TGACAACGGC	TTAACCCTATA	ACGGGCAAGC	CGTGAGCGTT	2880
AAAGATGGCG	GTTTAGTTGT	AGGCTTTAAG	GACTCTCAAA	ATCAATACAT	TTACACTTCC	2940
ATTCTTTATA	ATAAAGTGAA	AATCGCTGTT	TCTAATGATC	CTATCAATAA	CCCACAAGCC	3000
CCCACTTTAA	AACAATATAT	CGCTCAAATT	CAGGGCGTTC	AAAGCGTGA	TAGCATCGAT	3060
CAAGCTGGGG	GAAATCAAGC	GATTAATTGG	CTCAATAAAA	TCTTTGAAAC	TAAAGGAAGC	3120
CCTTTATTTC	CTCCCTATTA	TCTAGAGAGC	CACCTCCACAA	AAGATTTAAC	CACGATCGCT	3180
GGAGATATTG	CTAACACTTT	AGAAGTCATC	GCTAACCCCTA	ATTTTAAAAA	TGACGCCACT	3240
AATATTTTAC	AGATCAACAC	CTACACGCAG	CAAATGAGTC	GTTTAGCCAA	GCTCTCTGAC	3300
ACTTCAACTT	TGCGCCGTTT	TGATTTCTTA	GAACGCTTAG	AAGCCCTTAA	AAACAAGCGA	3360
TTCGCTGATG	CGATCCCTAA	CGCTATGGAT	GTGATTTTAA	AATACTCTCA	AAGGAATAGA	3420
GTTAAAAATA	ATGTGTGGGC	GACAGGAGTT	GGAGGGGCTA	GTTTCATTAG	TGGAGGTACT	3480
GGAACTTTAT	ATGGTATCAA	TGTAGGGTAT	GATAGGTTTA	TTAAGGGCGT	GATTGTGGGA	3540
GGTTATGCCG	CTTATGGGTA	TAGCGGGTTC	CATGCAAAACA	TCACTCAATC	AGGCTCTAGC	3600
AATGTCAATG	TGGGCGTTTA	TAGCCGAGCG	TTTATCAAAA	GAAGCGAGCT	AACCATGAGC	3660
TTGAATGAGA	CTTGGGGATA	CAATAAAACT	TTTATCAACT	CCTATGACCC	CCTACTCTCA	3720
ATCATCAATC	AGTCTTACAG	ATACGACACT	TGGACGACTG	ACGCTAAAT	CAATTATGGC	3780
TATGATTTCA	TGTTTAAAGA	TAAAAGCGTT	ATTTTAAAC	CCCAAGTAGG	CTTAAGCTAT	3840
TATTACATTG	GTTTGTCTGG	TTTAAGGGGC	ATTATGGATG	ATCCTATTTA	CAACCAATTC	3900
AGAGCCAATG	CTGACCCTAA	TAAAAAATCC	GTTCTAACGA	TCAATTTTGC	CCTAGAAAGT	3960
CGGCATTATT	TCAATAAAAA	CTCTTATTAT	TTTGTGATTG	CGGATGTGGG	CAGAGACTTA	4020
TTCAATTAAT	CTATGGGGGA	TAAAATGGTG	CGTTTCATCG	GTAATAACAC	CCTAAGCTAT	4080
AGAGATGGTG	GCAGATACAA	CACTTTTGCT	AGCATTATCA	CAGGCGGGGA	GATAAGATTG	4140
TTCAAAACCT	TTTATGTGAA	TGCGGGCATA	GGGGCTAGGT	TTGGGCTTGA	TTATAAAGAT	4200
ATTAATATTA	CCGGAATAT	TGGTATGCCG	TATGCTTTT			4239

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139

AGGGATAACA TGGAGCTTAT TTTAGGCTCT CAATCCAGCG CTAGGGCGAA TCTTTTAAAA	60
GAGCATGGGA TTAAGTTTGA ACAAAGCG CTCTATTTTG ATGAAGAAAG CCTAAAAACC	120
ACAGACCCTA GGGATTTTGT CTATTTGGCG TGCAAGGGGA AATTAGAAAA AGCTAAAGAG	180
TTACTTGCGA ATAATTGCGC TATCGTGGTG GCTGATAGCG TGGTGAGCGT GGGTAATCGC	240
ATGCAACGAA AAGCTAAAA CAAGCGAGAA GCCCTTGAAT TTTTAAAAACG CCAAATGGC	300
AATGAAATAG AGGTTTTAAC TTGCTCTGCA TTGATTCTC CTGTGTTGGA ATGGCTGGAT	360
CTATCGGTTT TTAGAGCGCG TTTAAAGCG TTTGATTGCA GCGAAATAGA AAAATATTTA	420
GAGAGCGGTT TATGGCAAGG AAGTGCGGGC TGTGTGCGTT TAGAGGACTT TCATAAGCCT	480
TATATTAAAA GCTCAAGCAA GAATTTAAGC GTGGGGTTGG GGCTGAATCT GGAAGGCTTG	540
TTAGGGGCAC TAAATTAGG GGTAAACTT TCATTATTA	579

(2) INFORMATION FOR SEQ ID NO:1140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140

AGAAATGGCTC TTTTGGTTC AAAGAGTAAG ATGTTAGAAA CTTATGCACT TAAAAGTGGG	60
GCTGTTTTTA TCTCTGATGC GCATTTTTTG CCCAAAAGCC CTCATTTAAT CCATACGCTT	120
AAAGAACTTT TAAGCGCCAA ACCCCGCAA GTCTTTTTCA TGGGCGATAT TTCCATGTT	180
CTTGTGGGCT ATTTACCCCT AGATAAAGAG CAGCAAAAA TCATTGATTT AATCCATGCG	240
TTGAGCGAAA TTTCACAAGT CTTTACTTT GAAGGCAACC ATGATTTTC CATGCGTTT	300
GTATTC AATT CCAAAGTAAT GGTTTTGAG CGCCAAAACC AACCCGATT ATTCCAGTAT	360
GATAACAAAC GCTTTTTGCT AGCCCATGGG GATTTATTCA TCACTAAAGC GTATGAATTT	420
TACATCACGC AGCTCACTTC CACTTGGGCT AGATTTTTTT TAACTTTTTT AAATTTATTA	480
AGTTTTAAAA CCTTATACCC TTTT	504

(2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 960 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

826

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141

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AATGATGATG AGAATAAAGT AATTGAATTA AAAACAAGGA ATAACATGCG CATCGTATTT      60
ATGGGAACGC CTAGTTTTCG TGAAGTGATC TTAAGGGCGT TGGTTGAAAA TGAAGATAAA      120
AAGATAGAAG TGGTGGGGCT ATTCACCTCA AGGGACAAAC CTTTGGGGCG CAAAAAAGAA      180
TTGAAAGCCC CAGAGACTAA AACATACATT TTAGAAAATC ATTTAAATAT TCCCATTTTC      240
CAGCCGCAAA GTTTGAAAGA GCCTGAAGTT CAAATCTTAA AAGGTTTGAA GCCTGATTTT      300
ATCGTGGTGG TGGCTTATGG TAAGATTTTG CCTAAAGAGG TTTTAACCAT CGCTCCTTGC      360
ATTAATTTGC ATGCGTCGTT ATTGCCCAAA TACAGGGGGG CTTGCGCCAT TCATGAGATG      420
ATACTCAATG ACGTAGGAT TTATGGCATA AGCACCATGC TTATGGATT TGAATTGGAT      480
AGCGGGGATA TTTTAGAAAG CGCTTCTTTT TTAAGAGAAG ATTATTTGGA TTTAGACGCT      540
TTAAGTTTAA AATTAGCGCG CATGGGGGCG ACTCTGCTTC TTTCAACGCT CAAAAATTTT      600
CATTCATCA CAAGAAAGCC TCAAGATCAC ATGCAGGCTA GTTTTTGTAA AAAAATCGCC      660
AAGGCCGATG GGTAGTGGG TTTTAAAGAC GCTAAAAACT TGTTTTTAAA ATCGCTTGCG      720
TTTTAAATCTT GGCCAGAAAT CTTTTTAGAA AATAGCCTTA AACTTTTAGA AGTGGAGTTA      780
GTGGAGAATG AAAAGAGCCA CAAGGAAGGC GAGATTTTAG CAATTGATGA AAGAGCGGTT      840
CTTGTAGGTT GTTTGAAAGG CAGCGTGCCT ATAGCAAGGT TGCAAGCGGT GGGTAAAAAG      900
CCTTTGAAAG CGAAGGATTA TTTGAATGGC AGGCGTTTGA AAGTGGGCGG TATTCTAACA      960

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(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142

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AAAAGCACAA GGAAACAAT AATGGAAGCG CAATTACGAT TTACGGGTGT TGGAGGGCAA      60
GGCGTGTGTG TAGCGGGAGA GATTTTAGCT GAGGCTAAGA TCGTGAGCGG GGGCTATGGC      120
ACTAAGACTT CCACCTACAC TTCGCAAGTG CGTGGAGGTC CCACTAAAGT GGATATTTTG      180
TTAGATAAAG ATGAAATTAT TTTCCCTTAT GCTAAAGAGG GCGAGATTGA TTTCATGCTT      240
TCAGTCGCTC AAATCAGCTA CAACCAAGTT AAAAGCGACA TTAAAAAAGG CGGTATCGTT      300
GTCATTGATC CCAATCTAGT AACCCCCACT AAAGAAGATG AGGAAAAATA CCAGCTTTAT      360
AAAATCCCTA TCATTAGTAT CGCTAAAGAT GAAGTGGGTA ACATTATCAC GCAATCTGTG      420
GTGGCGTTAG CCATTACCGT GGAGCTGACT AAATGCGTGG AAGAAAAATAT CGTTCTAGAT      480
ACCATGCTTA AAAAAGTTCC CTGCAAAAGT CGC                                513

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(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

827

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143

GCATGTTTAA	AACAAGAAAA	TATTACTAAT	ACGCAGATAT	TGCATATCGG	TGATAATTCT	60
TGGGCAGATG	ACGCTATGCC	TAAAAGTTTA	GGCATAGCAA	CGCTATTTAG	AAAAAGCGTG	120
TTGAAACAAT	TAGAAGAAGT	TTTTCCTAAA	TACAAAACAT	TTAATCCAAC	CAGTGTTCGG	180
CAAAGTTTTT	TTTATAGGATC	TTTATGCGTT	TTTTATAAAA	ATTATATTCA	AAAACATGAA	240
AAATTGATT	ATTGGTTTCT	TTTAGGAGCG	ATGCAGGCAG	GAATTGCAGC	CGTTGCTTAT	300
TGCCAGTTTA	TCTATAAGGA	GATTCACAAA	AGAAATATTG	ATACTTTAGT	GTTTGTTCGG	360
CGAGATGGTT	ATTTATTGCA	AAAAATTTTT	AATATTTTAT	ATCCAAATTC	ATATAAAACT	420
ACTTATGTCT	ATGCTCCCAG	AATTTTAAAA	AAAGCGGTAT	TTTTAGAAGT	CGTAGAGGGC	480
GAGAGTTTGG	AAATTTTGCG	TATTTTAGAA	GGCGAAGAAG	AAGTTAAAAA	GAAGCAAATC	540
ACCACCAACC	AACAGGCGTA	TGTATATCTC	TATAGCAATT	TTGAACATTG	CCGCCATTTA	600
GCGTTAAAAT	GTTTAGATAA	TTACAGAAAA	TACTTGTTTT	CATCAAATTT	AGAAGGAAAT	660
ATCGCTATTG	TAGATACGAT	TACTTTAGGC	TATTCTTCGC	AAGGGTTAAT	CCAAAAAGCT	720
TTAAATAAAG	AAGTTTTTGG	GTGCTATGTG	GATCTCCTAA	GAATTTTAAA	TTATGATTGC	780
GTGAGTTTCT	TACCTTTTTC	ACACCCTAAA	CCCGTTTATT	TTCAATAATTG	GGATTTTATG	840
GAGTTTTTGC	TAACAAGCCC	TGAATACCCT	ATTTTAAATG	TAGAAAATGG	CGTTCCAATC	900
TATCAAAAAG	ACGTTTCATC	TTGTGAAAAA	CACCGCTCTA	AAGCTTATGA	AAAAATAGTA	960
GAAGGGGCTG	TTGGATATGC	TTTCATATTT	AAAGAAAGTC	AAATTTCTTT	AGACATTCAT	1020
GATGTGATAG	AATGGGTGAA	TTCTTTCATT	GACAATCCTA	GTATTCAAGA	TCAAGAGCAA	1080
TTCAGACAAA	TTTATTTTCT	TCCAGACGCG	ACGCATAAAA	ACGCTCTGCC	CTTGTTTTGC	1140
AACGATGTTT	CTTTGTGTGC	TTGTATTTTA	AAGCCTTCAC	AAAGTTATAG	CGTATTAAAA	1200
AGGAGTCTTA	GGACAAACAA	GCAAGAGAGG	TTGTTTAAAA	TATTGTCTCT	AATTAAAAAA	1260
ATCTATGGGA	AGTTAAAAAA	GAAA				1284

(2) INFORMATION FOR SEQ ID NO:1144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144

GGGTTATTAG CTTGTTTGCT GGTCTTACTC AATCTAAAGA TTACGCCGAA TTTGATGTGG 60

SUBSTITUTE SHEET (RULE 26)

828

CCTTTAGATA	TTATTGTGGT	TGTGGCATGG	GTGTTATGGG	GGGTTAATAT	GTTTGGGAGC	120
ATGAGCGTTA	GAAGAGAGAA	TACTATTTAT	GTGTCCTTGT	GGTATTACAT	CGCTACTTAT	180
GTGGGTATAG	CGGTGATGTA	TATCTTCAAT	AACCTTTCTA	TCCCCACCTA	TTTGTGCGCT	240
GATATGGGGA	GCCTTTGGCA	TTCTATTTCT	ATGTATTTCAG	GCAGTAATGA	TGCGCTCATT	300
CAATGGTGGT	GGGGGCATAA	TGCGGTGCGT	TTTGTCTTTA	CGAGTGGGGT	GATTGGCAGC	360
ATTATTATT	TCTGCTTAA	AGAGAGCGGC	CAGCCTATCT	TTTCTTACAA	ACTCACTTTG	420
TTTTCTTTTT	GGAGTTTGAT	GTTTGTATTAT	ATTTGGGCGG	GCGGGCACCA	TTTGATCTAT	480
TCCACCGTGC	CTGATTGGGT	ACAAACCCCT	TCTAGCGTGT	TTTCAGTGGT	GTTGATCTTG	540
CCTTCGTGGG	GGACAGCGAT	TAACATGCTT	TTAACGATGA	GAGGCCAATG	GCACCAGCTC	600
AAAGAAAGCC	CTTTGATCAA	GTTTTTAGTT	TTAGCCTCAA	CTTCTACAT	GCTTCCACG	660
CTAGAAGGCT	CCATTCAAGC	CATTAAAAGC	GTGAACGCCT	TAGCCCACTT	CACCGATTGG	720
ATTATAGGCG	ATGTGCATGA	CGGCGTGCTT	GGGTGGGTAG	GCTTCACTTT	GATTGCGAGC	780
ATGTATCACA	TGACCCCTAG	GCTTTTCAAA	AGAGAGATCT	ATTCAGGAAG	ACTTGTGGAT	840
TTCCAATTTT	GGATCATGAC	TTTAGGGATT	GTGCTTTACT	TTTCGTCCAT	GTGGATTGCA	900
GGGATCACGC	AAGGGATGAT	GTGGAGGGAT	GTGGATCAAT	ACGGGAATCT	CACCTACCAA	960
TTCATTGACA	CGTTAAGGC	GCTAATCCCT	TATTACAATA	TTAGAGGCGT	TGGGGGTCTT	1020
ATGTATTTTA	TTGGATTTAT	TATTTTGTCT	TACAATATCT	TTATGACAAT	CACGGCAGGC	1080
AAAAAATTAG	AGCGTGAGCC	CAATTACGCC	ACGCCATATG	CCAGA		1125

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145

GGTTTTGATG	ACGATATGGA	AATTAGAAAC	ATCAAAGAGT	TTGAAAAAGC	TTCCAAAAAA	60
CTCCAAAAAG	ACACTTTAAA	GATCGCTCTC	GCTCTTTTGT	TCCTCATTGG	CGCCGCTTTG	120
CTCGCTCTCA	TTTTTGGGCA	GGCTAATTCT	AAGGGATTGT	TGCTCATCTT	TGCGGCCGTG	180
ATTGGGGGGT	ATATGGCGAT	GAATATTGGC	GCGAACGATG	TGTCTAATAA	TGTCGGCCCG	240
TCCGTAGGCT	CTAAAGCCAT	TAGCATGGGT	GGGGCGATTT	TGATCGCTGC	GGTTTGTGAA	300
ATGCTAGGAG	CGATCATTGC	TGGGGGGGAA	GTGGTTTCTA	CGATTAAAGG	CCGTATCGTT	360
TGCGCTGAAT	TTATTAACGA	TGCGCATGTT	TTCAATTAATG	TCATGTTGGC	TAGCCTTTTG	420
AGTGGGGCGT	TATGGTTGCA	TGTAGCCACT	TTAATAGGCG	CTCCCGTTTC	CACTTCGCAC	480
TCCGTAGTGG	GAGGGATTAT	GGGGGCTGGA	ATGGCAGCAG	CTGGAATGTC	TGCTATCAAT	540
TGGCATTTTT	TATCCGGCAT	TGTGGCTAGT	TGGGTAATCT	CGCCTTTAAT	GGGGGCTTTG	600
ATAGCCATGT	TTTTTTTAAAT	GCTCATTAAT	AAGACTATCG	CTTATAAAGA	AGATAAAAAG	660
AGCGCGGCTT	TAAAGGTCGT	GCCTTATTTG	GTGGCGTTGA	TGAGCTTAGC	CTTAGCTGG	720
TATTTGATCG	TGAAGTTTTT	AAAACGCCCT	TATGCGGTGG	GTTTTGAAAT	CCAGCTCGCT	780
TGCGGTTGTG	TCCTTGCCTG	TTTGATTTTT	ATCCTTTTAA	AAAGATTGTG	GTTAAAAAAA	840
GCCCCGCAAT	TAGAAAATAG	CCACGAAAGC	GTCAATGAGC	TTTTTAATGT	CCCTTTGATT	900
TTT						903

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs

SUBSTITUTE SHEET (RULE 26)

829

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146

AGAATGAAGC	TTAAAAAAC	CCTGACTTAT	CAACACCACG	CCTATTCTTT	TTTAAGCGAT	60
AACACGAATG	AAGTTTTAGA	AAACCCCTAAA	GAAATCCTTT	TTGTCAAAAC	GCCTTTAAAC	120
GAAAAATACG	CCCCTTTAAT	CGCAGAAAAA	AACCTGGCTA	TTTTGGATTT	TAACGAGCTT	180
AAAAACTACT	TTGATTTTAA	GATTAAGATT	GTAGGGATTA	CAGGCACTAA	TGGTAAAACG	240
ACCACAGCGA	GCTTGATGTA	TTCCTTGCTC	TTAGATTTGA	ATAAAAAGAC	CGCTCTTTTA	300
GGCACAAGAG	GGTTTTTTAT	CGACGACAAA	CACATCAAAG	AAAAGGGCTT	GACCACGCCC	360
ACTCTTTTAG	AGCTTTATAG	CGATTTGGAA	GAAGCGATTG	GTTTAAATG	CGAATACTTC	420
ATTATGGAGG	TGAGCTCCCA	TGCGATTGTC	CAAAAACGCA	TCGCTGGGCT	TGATTTGCGT	480
CTTAAAATTC	TCACCAATAT	CACAAGCGAT	CATTTAGATT	TCCATCAAAA	TATAGAAAAT	540
TACAGGGGACG	CTAAAAACAG	CTTTTTTAAA	GATGAGGGCT	TAAAAGTCAT	CAACAGAGAT	600
GAAACAAACG	CCCTTTTTTA	CCCCATTAAC	GCGCGCACTT	ACGCACTGGA	TAAAAAAGCG	660
CATTTGAATG	TTCAAGCCTT	TTCGCTCAAC	CCTTCCATTA	GCGCGTCTTT	ATGCTACCAA	720
CACGATTTAA	GAGATCCCAA	TCTTAAAGAA	ACCGCCCTGA	TCCATTCCCC	CCTTTTAGGG	780
CGTTACAACC	TTTATAATAT	TTTAGCGGGC	GTTTTAGGGG	TTAAATTGCT	CACTCAATTG	840
CCTTTAGAAA	CGATCGCACC	GTTATTGGAA	AACTTTTATG	GGGTAAAGGG	GCGTTTGGAA	900
ATTGTACATT	CTAAACCTTT	AGTGGTCGTG	GATTTTGCCC	ACACAACAGA	CGGCATGCAA	960
CAAGTTTTTG	AAAGCTTTAA	AAATCAAAAAG	ATCACCGCTC	TTTTTGGGGC	AGGGGGCGAT	1020
AGGGATAAAA	CCAAGCGCCC	TAAATGGGA	GCGATAGCGA	GTTGTTACGC	GCATCAAATC	1080
ATCTTAACTT	CAGACAATCC	TAGAAGCGAA	AACGAAGAAG	ACATCATTTA	GGATATTTTA	1140
AAAGGCATCA	ATAATTCTTC	TAAAGTCATT	GTAGAAAAAG	ACCGAAAAAA	GGCCATTTTA	1200
AACGCTTTAG	AAAATTTAAA	AGACGATGAG	GTGTTGTTGA	TTTTAGGCAA	GGGCGATGAA	1260
AACATTCAAA	TCTTTAAAGA	CAAAACGATT	TTTTTTT			1296

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 981 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147

SUBSTITUTE SHEET (RULE 26)

830

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AGATTATTAT CTCAATTTAA AACAAGGATA AACATGCAAG AATTCAGTTT GTGGTGCGAT      60
TTTATAGAAA GGGATTTTTT AGAAAACGAT TTTTAAAGC TCATCAATAA GGGGGCTATT      120
TGCGGGGCGA CGAGTAACCC TAGTTTGTGT TGCGAAGCGA TCACAAAAAG CGCGTTTTAT      180
CAAGATGAAA TCGCTAAACT CAAAGGCAAA AAAGCTAAAG AAATTTATGA AACTCTGGCA      240
CTAAAGGATA TTTTACAAGC CTCTAGCGCG TTAATGCCTT TGTATGAAAA AGACCCCTAAC      300
AACGGCTACA TCAGCCTAGA AATTGACCCC TTTTGTAGA AGCATGCGAT TAAAAGCATT      360
GATGAAGCCA AGCGGTTATT CAAAACATTA AACCGCCCCA ATGTGATGAT TAAAGTCCCG      420
GCGAGTGAAA GCGCTTTTGA AGTCATTAGC GCTCTGGCTC AAGCCTCTAT CCCCATTAA      480
GTAACCTTAG TCTTTTCGCC TAAAATTGCC GGTGAAATCG CTCAAATCTT AGCCAAAGAA      540
GCACGAAAAA GAGCGGTCAT TAGCGTGTGT GTCTCAGCAT TTGACAAAGA AATAGACCCA      600
CTAGTGCCAC AAAATTTGCA AGCTCAAAAGT GGGATCATGA ACGCTACCGA GTGTTATTAT      660
CAAATCAACC AGCATGCTAA TAAGCTAATA AGCACCCTTT TTGCATCCAC CGGCGTTAAA      720
TCTAATCTTT TAGCTAAAGA TTACTACATT AAAGCGCTGT GTTTTAAAAA CTCTATCAAC      780
ACAGCCCCCC TAGACGCCCT AAACGCTTAT TTGCTTGACC CAAACACCGA GTGTCAAACC      840
CCTTTAAAAA TCACAGAAAT TGAAGCGTTC AAAAAAGAAT TAAAAACGCA CAATATTGAT      900
TTAGAAAAAC CCGCCCAAAA ACTCCTTAAA GAAGGCTTGA TAGCGTTCAA ACAATCCTTT      960
GAAAAGCTTT TAAGCAGTTT T

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(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148

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GGGTTTAAAG TGCGTTTGTT TAGATTTGTG GGGTGGTATT ATTTCAAATA CTTTTAAATC      60
GTGCTTTTAG CTTTGGAATT GTTTTTTGTA GGCATTGACA GCCTGAAATA CGCCGATAAA      120
ATGCCCTGATT CTGCGAACAT GATCATTTTA TTTTTCACCT ATGATATTTT ATTCGCTCTC      180
AATTACACCT TGCCCATTTT CTGCTTTTGA GCGATGGTTT TATTTTATAT CACCTTCATT      240
AAATCCAACC AATACACCGC CCTGCTCTCT ATTGGATTTT CCAAATGCCA GATTTTAAGC      300
CCTATTTTTT TGATTAGCCT GTTTTTCACG GCTGTTTATG TGGGGTTGAA CGCGACTCCT      360
TTTGTGTATA TGAAGAAAAA AACGCAAAAT TTAATTATA AAGACAATTC TTTGAGCGTT      420
TCAGAGCATT TGTTAGTGAA ATACAACGAT GATTACGTGT ATTTTGATAA GATTAATCCC      480
TTATTGCAAA AAGCCCCAAA TATCAAGGTT TTTGCGCTAA AAGATAAAAC TTTAGAATCT      540
TATGCTGAAG CTAAAGAAGC TTTTTTGA GACAAATATT GGATTTTACA TGACACTACT      600
ATCTATGAGA TGCCCTTGAG TTTTGAACG GCGCGAACC CTTTAAACAC CACGCATTTA      660
GAAACCTTTA AAACGCTCAA AAATTTCCGC CCTAAAGTTT TAGACACCAT TTATCAAAAC      720
AAGCCTGCGG TTTCTATCAC AGACGCTCTT TTATCCTTGC ATGCTTTAGT GCGCCAAAAC      780
GCGGACACGA AAAAAGTGCG CTCGTTTTTG TATGTGTTTG CGATTTTGCC CTTTTTTGTG      840
CCGTTTTTAA GCGTTTTAAT CGCTTATTTT TCGCCAGTTC TCGCCCGCTA TGAAAACCTG      900
GCTCTTTTAG GGCTAAGTT TATCATTATC ACGCTCGTTG TTTGGGGGCT ATTCTTTGCT      960
TTAGGGAAGT TCAGCATTTT AGGATACTC ATTCTGAAA TAGGCGTTCT ATCGCCCTTT      1020
TTCGTATTTT TAGCTCTCAG TCTTTGTAT TTTAAAAAAC TTAATAAGAG ATTG      1074

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(2) INFORMATION FOR SEQ ID NO:1149:

SUBSTITUTE SHEET (RULE 26)

831

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149

AAGAGAAGAG	TGGTGAAATT	CTATACTTAT	AGTGGGGAAA	CGGCCGCTGA	AGCTTTAAAG	60
ATCGCTCAAA	GCCACCATGG	GGTGGATACG	CTGGTGTTTA	AAACCCAAGA	AATCCGTAAA	120
AAAACGCTCA	CTTCTTCTGG	GCTTTATGAA	ATCGTTGTGG	CGGTTGAAGA	AGAAGAAAAC	180
AAAAAAGCCC	CCCTCATTTCC	AGAGAGTTTG	TATGATGAAG	AATTGAATGA	AGAAGACGTG	240
GTCTGCAGC	TTTCAAGCAC	CGTAGAAGAA	ATGCGCAAAC	TCGCCGGGGT	TTCATCTAAC	300
CAGCGCAACT	ATACTTTTTC	AAAAAATAAG	ACTCTTTTAG	AAAAAGACGC	TCCATTAGAG	360
GATACGCCTT	TAGAGGCTAA	TAAGCAAGAC	GCCTTGTTGC	AAGCCTTAAA	AGATGAAGCC	420
AACCATAAAA	AAGAAAGAGA	AAAAAGAGAA	GTCAAACAAG	AAGAAGAAAT	TAAAGATATT	480
AATGCGCAAC	TAAGTAAAAT	CAGAGACAGC	TTAAACTCA	TTCAAACAT	GTTTTGGGAT	540
GAGAAAAACC	CTAATTCTGT	CAATATCCCT	CAAGAATTG	CCGAAATTTA	CAAACTAGCC	600
AAACAAAGCG	GCATGAAATC	CAGTCATTTA	GATGAAATCA	TGCAATTAAG	CCTGGAATTG	660
ATGCCTTTAC	GCATGCGGGA	AAATTCCCTA	ACGATCAAGC	GCTATTTTAG	AGAAGTGTTG	720
CGTAAAATAA	TCCTGTGTCG	CCCTGAAGAT	TTGAATTTGA	GGCAAAAACG	CATTTTAAATG	780
CTTGTAGGGC	CAACAGGCGT	GGGGAAAACG	ACGACTTTGG	CTAAATTAGC	CGCACGCTAT	840
TCTAGAAATG	TGGCTAAAAA	ATACAAGGTG	GGCATTATCA	CTTTAGACAA	TTATCGCATT	900
GGGGCTTTGG	AGCAATTGAG	TTGGTATGCT	AATAAAATGA	AAATGAGTAT	AGAAGCGGTG	960
ATTGACGCTA	AGGATTTTGC	TAAAGAAATT	GAAGCTTTGG	AATACTGCGA	TTTTATTTTA	1020
GTGGATACGA	CAGGCGATTG	GCAATACGAT	AAGGAAAAAA	TTGCCGGTTT	GAAAGAGTTT	1080
ATAGATGGGG	GTTATAATAT	TGATGTATCC	TTAGTGCTTT	CGGTTACCAC	TAAGTATGAA	1140
GACATGAAAG	ATATTATGTA	TTCTTTTGGG	GTGTTAGGGA	TTGACACTTT	AATCTTTACG	1200
AAATTAGATG	AGAGTAGGGG	GTTAGGGAAT	TTGTTTTCTT	TAGTGCATGA	AAGCCAAAAG	1260
CCTATCAGTT	ATCTTTCTGT	CGGCCAAGAA	GTGCCTATGG	ATTTGAAAGT	GGCTACTAAT	1320
GAGTATTTAG	TGGATTGCAT	GCTAGATGGC	TTTAGTAACC	CTAATAAGGA	ACAAGCA	1377

(2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1065 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

832

(B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150

ATCATGGCTG	ATATTTTAAAG	CCAAGAAGAA	ATTGATGCGC	TTTtagaAGT	CGTTGATGAG	60
AATGTGGATA	TTCAAAATGT	CCAAAAA	GATATTATCC	CCCAACGCAG	CGTAACCCCTC	120
TATGATTTC	AGCGCCCTAA	TCGTGTGAGT	AAGGAGCAAT	TGCGCTCTTT	TAGGAGCATC	180
CATGATAAAA	TGGCTAGGAA	TCCTTCCAGT	CAAGTCTCTT	CTATCATGCG	TTCTATTGTA	240
GAAATCCAGC	TTCATAGCGT	GGATCAAATG	ACTTATGGCG	AATTTTIGAT	GAGTTTGCCT	300
AGCCCTACGA	GTTTTAATGT	CTTTTCCATG	AAGCCTATGG	GGGGAACGGG	GGTTTTAGAG	360
ATTAATCCTA	GCATCGCTTT	CCCTATGATT	GACAGACTAT	TAGGGGGTAA	GGGGAGCGCG	420
TATGATCAAA	ACAGGGAGTT	TAGCGATATT	GAATTGAATT	TATTGGATAC	GATTTTACGC	480
CAGGTGATGC	AAATTTTAAA	AGAAGTGTGG	TCGCCTGTGG	TGGAGATGTA	TCCTACCATT	540
GACGCTAAAG	AATCCAGCGC	GAATGTGGTC	CAAATCGTCG	CTCAAAATGA	AATTTCTATC	600
ATGGTGGTTT	TAGAGATTAT	CATTGGGCAT	AGCCGTGGGA	TGATGAATAT	TTGTTACCCG	660
GTGATTTC	TTGAGAGCAT	TCCTTCTAAA	ATGGGGAGTA	GGGATTTCAT	GCTTTCAGAA	720
ACGAATCCA	AAAAGAGCCG	TAATAAGGAA	TTGCAAGCAC	TATTGAGCGG	GGTGAGCGTG	780
GATATGATGG	TGTTTTTGGG	CGCGGTGGAA	TTGAGTTTGA	AAGAAATGTT	CGATTTAGAT	840
TGCGGGGATA	CTATCCGGTT	GAATAAAGTC	GCTAACGATG	AAGTGAGCGT	GTATGTACAT	900
AAGAAAAAGC	GTTATTTAGC	GACCGTGGGG	TTTCAAGGGT	ATAGGAAAAC	CATTCAAATT	960
AAAGAAGTGG	TTTATAGCGA	AAAAGAACGC	ACTAAAGAAA	TTTTAGAAAT	GCTAGAAGAA	1020
CAGCGCAGAG	GCAAAAGTGGG	CGATATTATG	AAGATAGAAG	AAGAG		1065

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151

GGAACAAGCA	TGAGTAATCA	AGCGAGCCAT	TTGGATAATT	TTATGAACGC	TAAAAATCCC	60
AAAAGTTTTT	TTGATAATAA	GGGGAATACC	AAATTCATCG	CTATCACAAG	CGGTAAGGGG	120
GGCGTGGGGA	AATCCAACAT	TAGCGCTAAT	TTAGCTTACT	CTTTATACAA	GAAAGGTTAT	180
AAGGTAGGGG	TATTTGATGC	GGATATTGGT	TTAGCGAATT	TAGATGTCAT	TTTTGGGGTG	240
AAAACCCATA	AAAATATCTT	GCATGCCTTA	AAAGGCGAAG	CCAAATTGCA	AGAAATCATT	300
TGCGAGATTG	AACCCGGGCT	TTGCTTAATC	CCTGGGGATA	GCGGCGAAGA	AATTTTAAAA	360
TACATCAGCG	GCGCGGAAGC	TTTGGATCGA	TTCTAGATG	AAGAGGGGGT	TTTAAGCTCT	420
TTAGATTATA	TTGTGATTGA	TACGGGTGCT	GGGATTGGGG	CCACTACGCA	AGCGTTTTTG	480
AATGCGAGCG	ATTGCGTGGT	GATTGTTACC	ACACCCGATC	CTTCAGCGAT	TACCGATGCG	540
TATGCATGCA	TTAAATCAA	CTCCAAGAAT	AAAGATGAAT	TGTTCCCTTAT	CGCTAACATG	600
GTAGCCCAAC	CTAAAGAAGG	CAGGGCGACT	TATGAAAGGC	TATTCAAGGT	GGCTAAAAAC	660
AATATCGCTT	CATTAGAATT	GCACTATTTA	GGGCGGATTG	AAAACAGCTC	CTTATTGAAA	720
CGCTATGTGA	GGGAGCGAAA	GATTTTGAGG	AAAATAGCCC	CTAACGATTT	GTTTTGCGAA	780
TCCATTGACC	AGATAGCGAG	CCTTTTAGTT	TCTAAACTAG	AAACCGGCAC	TTTAGAAATA	840
CCAAAAGAAG	GTTTAAAAAG	CTTTTTTAAA	AGGCTTTTGA	AGTATTTGGG	G	891

(2) INFORMATION FOR SEQ ID NO:1152:

SUBSTITUTE SHEET (RULE 26)

833

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1593 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1593
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152

ATTTCGGAGT	TTAACCACCG	CAGTGC	CGCCT	TTAATCATT	ATTATGTGAA	TACCATTTTT	60
AAAAAAGCTT	ATCAAAATTC	ACCCACCGCT	TACTTGGAGC	AAAAATACCC	TAAAACTTCC	120	
AACAATAAAC	ATGTTACAGA	GGGCTATGTT	AAAGTCTCTT	TAGTGGCTGA	TGAAAAAGAA	180	
TTGTTATTAG	AACAAATCCT	ACAAGAAGCT	CAAAACCTTT	TAGAACATCG	TATTGATCCT	240	
AAAGACATTA	CCATTTTGTG	CGCCACCAAT	AAGGACGCTT	TAGAAATCAA	AAATTATTTG	300	
CAAGAGTATT	TGAGCGCAAT	TCGCCCAAGC	ACGGAATCTA	GCGCGAAATT	GTCTCAATTG	360	
GTAGAGTCTA	AAATCATTAA	GAACGCTTTA	GAATACGCTT	TAGCGGAAGA	ACCTTACAAG	420	
CCCTTTTATA	AACACAGTGT	TTTAAAACTC	GCTGGATACT	TGCATGATGA	TGTGATCGCT	480	
TTACCTGGTT	TTAACCCTAA	AAAAGAGAGC	GTGGCAAGCT	TTGTGTGGAA	AAATTATGGAG	540	
CAGTTTAAAC	TTTATGAAGA	GCCTGCGCAA	AGCTGTTTGG	AATTAGCGGT	TGGGTGCGAA	600	
GACGCCGATG	GATTTTGTAG	AAAATTAGAG	GCTAAAGAGA	TCGCTTCTTT	CAATCCAAAA	660	
GGCGCGCAGA	TCATGACCAT	TCATAAATCT	AAAGGCATGC	AATTCCCTTA	TGTGATTGTG	720	
TGCCAAGCCT	TGGGCAATCC	TAATTCAAGC	CATGCCAATC	AACTCCTTGA	AGAATATGAC	780	
GGCACAGAGC	TTGCGCGCCT	TTATTACAGA	ATGAAAAATC	GTGAGGTGGT	GGATAAAGAT	840	
TACGCCAGGG	CTTTAGACAA	AGAAGAAGCG	GCTAAAGATC	ACGAAGAAAT	TAATGTGTAT	900	
TATGTCGCAT	TCACTAGGGC	TGAGTTAGGG	CTGATTCTCG	TGGCCAAAGA	CAAGAAAGAA	960	
AGCAAAAAAG	AAAGCAAAAA	CAAAAAAATG	CACGAACAAT	TGGAACCTCG	ACCTTTAGAA	1020	
GAGGGAGAAA	TCGCGCCGGT	TATTTCTCCT	CAAAAAGAGC	CTTTAATGAC	AAGCGTTGTC	1080	
ATCAAGCCCC	ATGCCTATGG	CGAGCAAGTC	CAAGAAATAG	AAGAAGAGTC	AGATAGCGAT	1140	
TATGAAAAGA	ATAACGACCA	GGAAGCGATC	AATTTTGGTA	TCGCCTTGCA	TAAGGGATTG	1200	
GAATACCAAT	ACGCTTACAA	CATTCCTAAA	CAAAGCGTTT	TAGAATATTT	AAACTACCAC	1260	
TATGGTTT	ATGGTTTGG	TTACCAAGCG	TTAGAAGAAA	GTTTAGAGCT	TTTGTAAAAAC	1320	
GATGCAGGGA	TACAAGCCCT	TTTTAAAAAT	CATGCCCTTA	AGGGTGAAGC	GGCTTTTTTA	1380	
TTCCAAGGGG	TTGTGTCTAG	GATTGATGTT	TTATTGTGGG	ATAGAGGGCA	AAATTTGTAT	1440	
GTTTTAGATT	ATAAAAGCTC	TCAAAATTAC	CAGCAAAGCC	ATAAAGCGCA	AGTGTCTCAT	1500	
TACGCTGAGT	TTTTGCGAAC	TCAAGCCCCC	CATTTTAAGA	TACAAGCGGG	CATTATTTAC	1560	
GCTCATAAAA	GACTGCTTGA	AAAATTATGG	GTT			1593	

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

834

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153.

TTATCAACCG	CTTATCAGGC	GGTAGAACTC	CATTGGTTCC	TGAAAGCTGT	TCTAGTCCTG	60
GAGCGATCAC	CATCTTCACC	AGAAATAAAA	GGTATTGGG	ATAGGGATTA	CCACACGCCT	120
ATCACCAGTT	CTTTCACCCT	TGATGTGAGC	TATGACAACA	CCGATGATTA	TTATTTCCCT	180
AGAAATGGGG	TTATCTTTAG	TTCCTATGCG	ACAATGTCTG	GTTTGCCAAG	CTCTGGCAGC	240
CTCAATTCTT	GGAACGGGTT	AGGCGGGAAT	GTCCGTAACA	CCAAAGTTTA	TGGTAAATTC	300
GCCGCTTACC	ACCATTTGCA	AAAATATTTA	TTGATAGATT	TGATCGCTCG	TTTAAAACG	360
CAAGGGGGCT	ATATCTTTAG	GTATAACACC	GATGATTACT	TGCCCTTAA	CTCCACTTTC	420
TACATGGGGG	GCGTAACCAC	GGTGAGAGGC	TTTAGGAACG	GCTCAATCAC	ACCTAAAGAT	480
GAGTTTGGCT	TGTGGCTTGG	AGGCGATGGG	ATTTTACC	CTTCTACTGA	ATTGAGCTAT	540
GGGGTGTTAA	AAGCGGCTAA	AATGCGTTTA	GCGTGGTTTT	TTGACTTTGG	TTTCTTAACC	600
TTTAAAACCC	CAACTAGGGG	GAGTTTCTTC	TATAACGCTC	CCACCACGAC	GGCGAATTTT	660
AAAGATTATG	GCGTTGTAGG	GGCTGGGTTT	GAAAGGGCGA	CTTGAGGGGC	TTCTACAGGC	720
TTACAGATTG	AATGGATTTC	GCCCATGGGG	CCTTGGTGT			759

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154

GCGAGGATCA	TGCTTGATAA	ACGCATTAAA	ACGCTTTTAC	TTTTTTTTTG	TCTTAATATG	60
GTGTGTTTGA	GCGTGAGTTT	TACCAATAAG	CCTCATTGT	GTTTTTGTTT	TTAGTGTTA	120
GGTTGTTATT	TAGTTTATGA	GTGGCAAAAG	AAACAAAAAA	AAGATTTTCA	AAGCGCTAAA	180
AGTTTGAAAT	TTGACAGCGT	TAGCGAATTA	GAAAAGGATT	TGAACATGGA	AGTAACTAAT	240
GATGAATGGG	ATACCCAT					258

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

835

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155

TCACGGAGTG	TTGAAATGAA	CTACCCTAAT	CTACCTAACA	GCGCTTTAGA	GATAAGCGAA	60
CAGCCAGAAG	TGAAAGAAAT	CACTAACGAG	CTTTTAAAGC	AATTACAAAA	CGCTTTAAGG	120
AGCAACGCGC	ATTTTAGCGA	GCAAGTGGAA	TTAAGCCTTA	AATGCATCGT	TAGGATTTTA	180
GAAGTGCTTT	TGAGTTTGGG	TTTTTTTAA	AATGCGAATG	AGATTGATAG	CAGTTTAAGA	240
AATTCATTG	AGTGGCTGAC	TAACGCCGGC	GAGAGCTTGA	AATTAAAAAT	GAAAGAATAC	300
GAGCGCTTTT	TTAGCGAGTT	TAATACGAGC	ATGCATGCCA	ACGAGCAGGA	AGTAACCAAT	360
ACCTTAAACG	CTAACGCCGA	GAACATTAAA	AGCGAAATTA	AAAAGCTAGA	AAATCAATTG	420
ATAGAAACCA	CGACAAGACT	TTTAACGAGC	TATCAAATCT	TTTTAAACCA	AGCCAGAGAT	480
AACGCTAACA	ACCAAATCAC	AAAAAACAAA	ACCCAAAGCC	TTGAAGCGAT	TACACAAGCT	540
AAAAACAACG	CTAATAATGA	AATAAGCAAC	ACTCAAACGC	AAGCGATAAC	TAATATCACC	600
GAAGCGAAAA	CGAACGCTAA	TAATGAAATA	AGCAACAATC	AAACGCAAGC	GATAACTAAC	660
ATTAACGAAG	CCAAAGAAAG	CGCTACAACG	CAAATAAACG	CCAATAAGCA	AGAAGCAATA	720
AATAACATCA	CGCAAGAAAA	AACCCAAGCC	ACAAGCGAGA	TCACCGAAGC	GAAAAAGACC	780
GATCATTATC	AAAACATTGA	TTTTTTTGAG	TTTGAA			816

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156

GGATTGTCGG	TGTTAGAACG	CTATGCGAAT	GAAGAAATGA	AAGCCCTATG	GAATGAGCAA	60
ACCAAATTTG	AAACTTATTT	GGAAGTGGAA	AAAGCTGTCT	TTAGGGCGTG	GAATAAGCTT	120
GGGCAAATTC	AAGATAGCGA	TTGTGAAAAA	ATCTGCTTAA	AAGCGGCATT	CAATCTTGAA	180
CGCATCAAAG	AAATTGAAAA	AACCACTAAG	CATGATTTAA	TCGCTTTCAC	TACTTGCGTG	240
GCTGAAAGCT	TGGGCGAAGA	ATCCCGCTTC	TTTCATTATG	GGATCACTTC	TAGCGATTGC	300
ATTGATACGG	CTATGGCGTT	ATTGATGACC	AAAAGCTTAA	AACTCATTCA	AAAAGGCGTT	360
AAAAACCTCT	ATGAAACCTT	TAAAAATAGG	GCTTTAGAGC	ATCAAGACAC	GCTAATGGTG	420
GGCAGAAGCC	ATGGGGTGTT	TGGCGAACCC	ATCACCTTTG	GTCTAGTTTT	AGCTCTTTTT	480
GCTGATGAAA	TCAAACGGCA	TTTAAAAGCC	CTGGATTTAA	CGATGGAATT	TATCAGCGTA	540
TGGGCGATCA	GTGGGGGTCT	CGGGAATTTC	GCGCACGCCC	CTTTAGAATT	AGAAGAATTA	600
GCGTGCGGAT	TTTTAGGCTT	AAAAACCGCT	AATATCAGCA	ATCAAGTCAT	TCAAAGAGAC	660
CGCTACGCTA	GGCTTGCAAT	CGATCTGGCT	CTTTTAGCGA	GCAGTTGTGA	AAAAATCGCT	720
GTCAATATCC	GCCATTTGCA	ACGCAGTGAA	GTCTATGAAG	TGGAAGAAGC	TTTTTCAGCA	780
GGGCAAAAAG	GAAGCTCTGC	GATGCCTCAT	AAAAGAAACC	CCATCTTGAG	CGAGAATATC	840

SUBSTITUTE SHEET (RULE 26)

836

ACCGGGCTTT	GCAGGGTGAT	TCGCTCTTTT	ACTACCCCA	TGCTAGAAAA	TGTCGCCTTA	900
TGGCATGAAA	GGGACATGAG	CCATAGCTCT	GTGGAGCGTT	TTGCGCTGCC	TGATCTGTTT	960
ATCACCAGCG	ATTTCATGCT	CAGCCGTTTG	AATAGCGTGA	TTGAAAATCT	GGTGGTTTAT	1020
CCTAAAAACA	TGCTTAAAAA	TTTAGCTTTG	AGTGGGGGGC	TAGTCTTTTC	GCAACGGGTG	1080
TTATTGGAAT	TGCTTAAAAA	AGGTTTGAGC	AGAGAAGAAA	GCTATTCTAT	CGTGCAAGAA	1140
AATGCCGATGA	AAATATGGGA	GGTTTTCGAA	CAAGGCGCTT	TTAAAAACGC	TGATGAAAAT	1200
TTATTTTAA	ACGCCCTACT	TAACGATGAA	CGCTTGAAAA	AATATTTGAA	TGAGAGCGAA	1260
ATCAGAGCAT	GTTTTGATTA	CAGCTATTAC	ACTAAAAATG	TGGGGCGCAT	TTTTAAAAGG	1320
GTGTTTGGA						1329

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157

AATGATAGTG	GCTCAAAACA	TTTCATCTTG	CCTTTTTTAA	CGCTCCTTTT	GCAAATGTAT	60
TTGAGCCGCA	CACGAGAATA	CATGGCCGAT	AGCGGGGCGG	CGTTTTTAAT	GCATGACAA	120
AAGCCCATGA	TCAGAGCCTT	ACAAAAGATT	TCTAACGATT	ACACCAACAA	CGATTATAAA	180
GAAATAGATA	AAAATAGCAC	CCGATCAGCG	GCCTATCTTT	TTAACGCTGA	AATGTTTAGC	240
ACCCACCCTA	GTATTAAAAA	TCGTATCCAA	TCCTTAAGAA	AGCGTGTGAT	C	291

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158

ATGGAAAAAT	TTTTCAACCA	ATTTTTTGAA	AACATCGGCG	AAGACAAGAA	TCGAGAAGGT	60
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SUBSTITUTE SHEET (RULE 26)

TTGAAAGAGA	CGCCTAAAAG	GGTTCAAGAA	TTATGGAAAT	TCTTGATATA	A-----	120
GAAGATCCTA	GAGTGGCTTT	AAAAAGCGCG	TATTTTCAAG	GCGTTTGCGA	TGAAATGATA	180
GTGGCTCAAA	ACATTGAATT	TTACTCCACT	TGCGAGCACC	ATTGCTCCC	TTTTTTGGG	240
AATATTAGCG	TGGGATATAT	CCCTAAGGAA	AAGATTGTAG	GCATTAGCGC	GATCGCTAAA	300
CTCATTGAAA	TTTATAGCAA	ACGCTTGCAA	ATCCAAGAAA	GGCTGACCAC	TCAAATTGCA	360
GAAACTTTTG	ATGAAATCAT	AGAGCCAAGG	GGCGTGATCG	TGGTTTGTGA	AGCCAAGCAC	420
TTGTGCATGA	GCATGCAAGG	GGTGCAAAAG	CAAAATGCGA	TCATTAAAAC	AAGTGTGTTA	480
AGAGGCCTCT	TCAAAAAAGA	CCCTAAAACC	AGAGCTGAAT	TTATGCAACT	CTTAAATCT	540

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159

GTTATAATTC	TAGGCATGAG	TAACCCTAAT	TTATCCTTTT	ATTGTAATGA	GTGCGAGCGT	60
TTTGAAAGCT	TTTAAAAAA	CCATTATTTA	CACCTTGAAG	GCTTCCACCC	TTATTTGGAA	120
AAAGCCTTTT	TTGAAATGGT	GCTTAATGGG	GGCAAAAGGT	TCCGCCCCAA	GCTTTTTTTA	180
GCCGTGCTTT	GCTCTTTAGT	GGGTAAAAAA	GATTATTCTA	ACCAACAAAC	AGAATATTTT	240
AAAATCGCTT	TAAGCATTGA	ATGCTTGCAC	ACTTATTCGC	TCATCCATGA	CGATTTGCCT	300
TGCATGGATA	ACGCTATTTT	AAGAAGAAAC	CACCCCACTT	TACACGCCAA	ATACGATGAA	360
ACCACAGCCG	TTTTAATCGG	CGATGCGCTC	AACACCTATT	CTTTTGAATT	GCTCTCAAAT	420
TCTTTACTAG	AAAGCCGTAT	CATTGTGGAA	TTAGTCAAAA	TCCTAAGCGC	TAATGGGGGG	480
ATTAAAGGCA	TCATTTTAGG	GCAGGCTTTG	GATTGCTATT	TTGAAAACAC	CCCCTTAAAT	540
TTAGAGCAGC	TCACTTTCTT	ACACGAGCAT	AAAACCGCTA	AATTGATTAG	CGCAAGCCTG	600
ATTATGGGGC	TTGTTGCGAG	CGGCATTAAC	GATGAAGAGC	TTTTAAAATG	GCTTCAGGCT	660
TTTGGGTTAA	AAATGGGTCT	TTGTTTTCAA	GTGCTAGATG	ATATTATAGA	CGTTACACAA	720
GATGAAAAAG	AAAGCGGTAA	AACCACGCAT	TTAGACAGCG	CTAAAAACAG	CTTTGTGAAT	780
TTATTGGGGC	TAAAAAAGGC	AAGCGGTAC	GCCCCAACTT	TAAAAACAGA	GATTTTAAAC	840
GATTTGAATG	CATTAGAACC	TACTTATCTT	TCATTGCAAG	AAAATTTAAA	CGCATTATTG	900
AACACTCTAT	TTAAAGGCAA	GACA				924

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

838

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1041
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160

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CTTCTCAATA CATCAAAGAA AAAGCGCAAT TTGAATTGGA ATTTTACTTG CCTAAAGGGA      60
GTTATGCGAG CGCGCTGCTC AAAGAAATCA AGCATGAGAA AGGAGAAAAT AATGACGAAT      120
TTTGAAGAAGA TTATCGCGCA AAACAGGCTC AAAACGAACG CGGTTTTAAC CACTTACTGC      180
GCGATTTTTG CTTTTATTGG GTTGTGGTGG GATGCTATTA GAATCAACGC TAATGATTTA      240
GGTATAGCCC TTTTAAACT CATGACTTTT CAAATTTTTC CTACGATTAC TATTGTTCATG      300
TTTGTGGTGG CTTTTGTCAT TATTCTTGTT TGTATCCAAA ATTTTAGCTC TATCATGTTA      360
AGCGGCGATG AATACAAGCT TATTGACCCA AGCAAGGTTT TAAGCTCTAA AGAAAATCAA      420
ATCCATCGCC TTTTGTAGA GCTTTTAGAA GAGGCTAAGC TTCATTTTGA GCCTAAGCTT      480
TATATCATT ACGCCCTTA CATGAACGCT TTTGCGAGCG GGTGGGATGA ATCTAATTCC      540
CTTATCGCTC TTACAAGCGC TTTAATAGAG AGTTAGATA GAGACGAATT AAAAGCCGTG      600
ATCGCTCATG AGCTCAGCCA CATACGGCAC AACGACATCC GCTTGACCAT GTGCGTGGGG      660
ATTTTGAGCA ATATCATGCT ATTGGTGGCT AATTTTAGCG TGTATTTTTT CATGGGGAAT      720
CGCAAGAATA GCGGGGCGAA TTTAGCCCGA ATGATTTTAT GGGTTTTACA GATCATCTTG      780
CCTTTTTTAA CGCTCCTTTT GCAAATGTAT TTGAGCCGCA CACGAGAATA CATGGCCGAT      840
AGCGGGGCGG CGTTTTTAAT GCATGACAAT AAGCCCCATGA TCAGAGCCTT ACAAAGATT      900
TCTAACGATT ACACCAACAA CGATTATAAA GAAATAGATA AAAATAGCAC CCGATCAGCG      960
GCCTATCTTT TTAACGCTGA AATGTTTAGC ACCCACCCTA GTATTAAAAA TCGTATCCAA     1020
TCCTTAAGAA AGCGTGTGAT C                                     1041

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(2) INFORMATION FOR SEQ ID NO:1161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161

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ACACAGCCAC ACAAAAACAA GAGATTAAAC AAGAGATTAA ACAAGAGATT AAACAAGAGA      60
TTAAACAAGA GATTAAACAA GAGATTAAAC AAGAGATTAA ACAAGAAACT AAACAAGAGC      120
AAGAAAAAGA AAATAAGCCT AAACAAAACA GTGTCTCGCC CGTTCAAAAC GATCAAAAAA      180
CCCCCACAAC CCCCT                                     195

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(2) INFORMATION FOR SEQ ID NO:1162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162

GGGGTAAACA TGCTTATTTT AGGACACCCCT TTAATCCCTA GCGCTCGTTT TGTTTTCATT	60
AAAAACACCG ATGCTATTCA TTCCAGCGCC AATAACGATA TAGTGTGTTT TGAAGCAAAC	120
CCAAAAAATT TGGAAATTAGC CCAATATTGC TGTGAAAATG GCGTCCATTT TAGCGTGATC	180
TTTTTATCGC ACAAGATAGA GACGGACACC TTTTITTTAT TCAACGCTTT CAAACCGCTC	240
TATTGTATT TTAAGGATAT TAAGCAAGCC ATACTCGCCC AACACACGC CACTAATTAC	300
TTGTTAGATA GCAAAATCTT GTTTTCTATG GATTTTAACG ATACAGAGTC ATGGGAGATT	360
TGCCTAATA ATCAAATAGA TGGTGTCATT TCTAAAGATT CACTCCTTTT GAAA	414

(2) INFORMATION FOR SEQ ID NO:1163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163

TTTAAATGCA ATCTTAAAG GAGAAGTGCT TTGAACTAC TGGTAGTAGA TGATAGCTCA	60
ACTATGAGAA GAATTATTAA AAACACACTT TCACGCTTAG GCTATGAAGA TGTTTTAGAA	120
GCTGAGCATG GGGTGAAGC TTGGGAAAAA CTAGACGCTA ATGCGGACAC TAAGGTGCTT	180
ATTACGGATT GGAACATGCC TGAAATGAAC GGGTTGGATC TCGTTAAAAA GGTGCGTGCG	240
GATAACCGAT TTAAGGAAAT CCCTATCATT ATGATCACCA CAGAGGGCGG TAAAGCTGAG	300
GTCATTACGA CTTTAAAGC GGGCGTGAAT AACTACATTG TGAAACCTTT TACCCCCCAA	360
GTTTTGAAAG AAAAATTAGA GGTGTTTTTA GGGACAAACG AT	402

(2) INFORMATION FOR SEQ ID NO:1164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

840

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164

CGGGTTATGG	CGGTGCGAAT	CATGGCGACG	GATGAGACAA	ACTCATGCAA	GGAATTTGGA	60
CTCGTATCGC	TCCTTTTAAG	CTTGTTGGTG	CTAGTGGTGG	TGGGGCGTTT	TTTCATTAAAG	120
GGGGCGTTT	ATGGGCTAAA	AAATGGCGTT	TGGGCGATGG	ATTTGAGCGT	GTCTTTTGGG	180
GCGTTGTCCG	CGTTTGTTTA	TTCCCTTTAT	GCGATGTTGG	TGTCTCAAGA	GACCTATTTT	240
GAAGCGAGCA	GCACGATTTT	AACGCTTGTT	TTTGGCTCTA	AGTTTTTGA	ATTAAAGGCT	300
AGGCTGTTTG	CGAATGAAAA	ATGCTGGGCC	CTAGAAATCGC	ATGAAATCCA	TAGCGTGATC	360
GTTGTAGAAA	ACGGCAAGCA	GATAGAAAAA	CACCCTAAAG	ATGTGGCGAT	AGGCTCGGTT	420
GTCTGGGTGC	CAAGCGGGGC	TAAATCGCT	TTAGATGGCG	TGCTTTTAA	TAGCGCGAGC	480
GTGGATGCGT	CTTGTATCAG	CGGGGAGTTT	AAGCCTTTGG	AATTGGGGGT	TAATGATCCA	540
ATTTTAGGGG	GTTATGTGAA	CGTGGGCGTG	CCTTTTAGCT	ATCAAGTGAG	CGCGACCTTT	600
CAAACTCAC	GCCTTCTAG	TTTGTAGAA	ACTTTAAAAA	AGAGTTTTTT	AGAAAAGCCC	660
TTAATTGAGA	GCAGCGCGAA	TAAATCGCG	GATATTTTTT	CTAAAGCGGT	GTTGTTTTTA	720
GCCTTTGTGA	GCTTTTATT	GTGGCAATTT	GGTTTGGGGG	GTAATTTTGA	AAAAGCTTTA	780
ATGGTGTGTA	TTAGCGTGCT	AGTCATAAGC	TGCCCTTGCG	CGTTCGCTCG	GCTACGCCCA	840

(2) INFORMATION FOR SEQ ID NO:1165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165

CGTGCTAGTC	ATAAGCTGCC	CTTGCGCGTT	CGCTCGGCTA	CGCCCATAGC	GTTAGTGATA	60
GGGGTGTTTA	AAAACCTTTT	GATCGTGTTT	AAAGAAGCGT	TGTTTTTAGA	AACTCTGGCT	120
AAAGTGAAAA	AAATCTTTAT	AGACAAAACC	GGCACCCTCA	CGCAAAAAGA	AGTCCTTTTA	180
AAAGAAAAAA	TCATTTCATGA	AGAATTTGAT	GAAAGGCTTT	TAAAGAGCCT	TTTAAAAACT	240
AGGGAGCATT	TAGCCCATAA	TGCGATTCTT	AAACATTAG	ATGGCGATGA	GGTTGATTTG	300
GAAAAGATAG	AGTTTTTCGC	TCATGGCCTG	AAAGCGAGCT	ATCAAAACGA	AACCTTGCTA	360
GTGGGGAGTT	TGAAATTTTT	AAACGCTATG	GGGGTTGATT	TAAAGGTTAA	AGAGAGCGCT	420
AATATCATGG	TAGGCTTTGC	GAAAAATAAG	ACCTTATGCG	CGTTATTCAT	TTTAGAAGAG	480
CGTTTGAAAG	CTAACGCTAA	AGAAGTCATT	CAGGCTTTAC	AAAATCAAGG	CTTGGAATTA	540
GAAATTTTAA	GCGGGGATAA	TGAAAGCTCG	GTAAAGGAGT	GCGCGAAA		588

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:1166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2001 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166

ACCCCAACCA	AAGCCCTTAA	AATCGTGCAA	GAGCAGGTTA	CTTACCCGTT	GGTTTCTACT	60
TTCATGAGTA	TCGCTAACAT	TGACACGGTT	AGAGGGATTT	CTAGCTATGA	AAGCGGCTTG	120
ATTTACATCA	TTTTTAAAGA	CGGCGTCAAT	TTGTATTGGG	CTAGAGATAG	GGTTTTAGAG	180
CAATTAACA	GAGTAAGCAA	TCTGCCTAAG	GACGCTAAAG	TGGAAATAGG	GAGCGATTCC	240
ACTTCTATTG	GCTGGGCGTA	TCAATACGCT	TTATCTAGCG	ATAGCAAGAA	TTTAAGCGAT	300
TTGAAAGTCT	TGCAAGATTT	CTATTACCGC	TATGCGCTTT	TGGGGGTGTA	TGGGGTGAGT	360
GAGGTCGCGA	CGGTGGGGGG	CTTTGTGAAG	GATTATGAAG	TAACGCTTCA	AAACGATTCT	420
TTGATCCGTT	ATAACTTGAG	TTTAGAACAA	GTCGCTAACG	CGATTAAAAA	TTCCAATAAC	480
GATACCGGTG	GGGCGGTTAT	TTTAGAAAAC	GGGTTTGAAA	AAATTATAAG	ATCGCATGGC	540
TATATCCAAT	CTTTAAACGA	TTTAGAAGAA	ATTGTGGTTA	AAAAAGAAGG	GGCTATCCCT	600
TTAAAAATCA	AAGATATAGC	GAGCGTTAGG	CTAGCGCCCA	AACCGCGCAG	AGGGGCGGCT	660
AATCTCAACG	GCGATAAGGA	AGTGGTGGGC	GGGATTGTTA	TGGTGGCGTA	TCACGCTGAC	720
ACTTATAAGG	TGCTTAAAGC	CATTAAAGAA	AAAATCGCCA	CCTTACAAGC	GAGTAACCCCT	780
GATGTGAAAA	TCACCAGCGT	GTATGACAGG	AGCGAATTGA	TTGAAAAAGG	CATTGACAAT	840
TTGATTCCAC	CGCTCATAGA	AGAAAGCGTC	ATTGTGCTAG	TCATTATTGC	GATTTTCTTA	900
CTGCATTTCA	GGAGCGCTTT	AGTGGTGATT	ATCACTCTGC	CTTTAAGCGT	GTGCATCAGT	960
TTCTTGCTCA	TGCGTTATTT	CAATATTGAA	GCGAGCATCA	TGAGTTTGGG	GGGCATTGCG	1020
ATCGCTATAC	GGGCGATGGT	GGATGCGGCG	ATAGTGATGG	TGGAGAACGC	TCACAAGCAT	1080
TTGCAACACA	TTGACACGAG	AGACAACACT	CAAAGGGTTA	ATGCCATCAT	GCAAGGGGTT	1140
AAGCATGTGG	GGGGCGCGAT	ATTTTTTGCG	TTAATGATCA	TCGTGGTTTC	TTTCTTGCCT	1200
ATTTTCGCGC	TCACCGGTCA	AGAAGAAAAG	CTTTTGCCCC	CTTTAGCTTA	CACCAAAACC	1260
TTTGCCATGC	TAGTGGGAGC	GCTGCTTTCT	ATTACGATAG	TCCCTGTTTT	AATGGTATGG	1320
CTCATTAAAG	GGCGGATTTT	AGAAGAGTCC	GAAAGCCCCG	TTAACGCTTT	TTTCATGAAA	1380
ATTTATGGCG	TGAGTTTGAG	GGTTGTGCTT	AAGTTCAGAT	ACGCTTTTTT	AATAGCGAGC	1440
GTCTTAGGTT	TAGGGGGTTT	AGTTGTAGCG	TATAAAAAAC	TCAACTGGGA	ATTTATCCCC	1500
CAAATCAATG	AAGGGGTAAT	CATGTATATG	CCTGTAACCTA	TTAATGGCGT	GGGTATTGAT	1560
ACCGCTTTAG	AATATTTGAA	AAAAAGTAAC	GCTGCTATCA	AGCAACTGGA	TTTTGTCAAA	1620
CAGGTTTTTG	GTAAAGTGGG	GCGCGCTAAC	ACCAGCACCG	ATGCCGCCGG	TTTAGGAATG	1680
ATAGAAACCT	ACATTGAATT	AAAGCCGCAA	AACGAATGGA	AAGAAAAGCT	CAGCTATAAA	1740
GAAGTTAGGG	ACAAATTGGA	AAAAACCCTG	CAATTAAGAG	GCTTGACTAA	TTTCATGGACT	1800
TACCCCATTC	GTGGCAGAAC	GGACATGCTC	TTAACCGGCA	TTAGAACGCC	CCTAGGCATC	1860
AAGCTCTATG	GTAACGACAC	GGACAAATTA	CAAGAATTGG	CGATCCTTAT	GGAGCAACAG	1920
CTCAAAACCC	TCAAAGAGAG	TTTGTCCGGC	TTTGCCGAGC	GATCCAATAA	CGGCTACTAC	1980
ATCACGCTGG	ATTTGGAACG	A				2001

(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

842

- (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167

CGCAACGTGG	AAGCGCGTTA	TTATTATGGG	GACACTTCAT	ACTTTTATTT	GCATGCGGGA	60
GTTTTACAAG	AGTTCGCTCA	CTTTGGATCG	AATGATGTGG	CGTCTTTAAA	CACCTTTAAA	120
ATCAATGCCG	CTCGCAGTCC	TTTAAGCACC	TATGCAAGAG	CGATGATGGG	TGGGGAATTG	180
CAATTGGCTA	AAGAAGTGTT	TTGAATTTG	GGCGTGGTTT	ATTTGACAA	TTTGATTTC	240
AACGCAAGCC	ATTCGCTTC	CAATTTAGGA	ATGAGGTATA	GTTC		285

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168

AAACCTACCA	ATGTTTGGGC	TAACGCTATT	GGGGGAGCGA	GCTTGAATAG	CGGCTCTAAC	60
GCTTCATTGT	ATGGCACAAG	CGCCGGCGTA	GACGCTTTCC	TTAACGGGAA	TGTGGAAGCC	120
ATTGTGGGCG	GTTTTGGAAG	CTATGGTTAT	AGCTCCTTTA	GCAATCAAGC	GAACTCTCTT	180
AACTCTGGGG	CCAATAACGC	TAATTTTGGC	GTGTATAGCC	GTTTTTTTGC	CAACCACCCT	240
GAATTTGACT	TTGAAGCTCA	AGGGGCGCTA	GGGAGCGATC	AATCAAGCTT	GAATTTCAAA	300
AGCACTCTAT	TACAAGATTT	GAATCAAAGC	TATAATTACT	TAGCCTATAG	CGCCACAGCA	360
AGAGCGAGTT	ATGGTTATGA	CTTCGCGTTT	TTTAGGAACG	CTTTAGTGTT	AAAACCAAGC	420
GTGGGCGTGA	GCTATAACCA	TTTAGGTTCA	ACCAACTTTA	AAAGCAATAG	CCAATCACAA	480
GTGGCTTTAA	AAAATGGCGC	GAGCAGTCAG	CAATTATTCA	ACGCTAACGC	AACGTGGAAG	540
CGCGTTATTA	TTATGGGGAC	ACTTCATACT	TTTATTTGCA	TGCGGGAGTT	TTACAAGAGT	600
TCGCTCACTT	TGGATCGAAT	GATGTGGCGT	CTT			633

(2) INFORMATION FOR SEQ ID NO:1169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs

SUBSTITUTE SHEET (RULE 26)

843

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169

AATAAAATCC TAGCCAGTGA GCTAGAATTT AAATTTTAA TCAAAGGAGT CATCATGGCA	60
CACCATGAAG AACAACACGG CGGCACACCAC CACCATCACC ACCACACACA CCACCACCAT	120
TATCATGGCG GCGAACACCA CCATCACCAC CACAGCTCTC ATCATGAAGA AGGTTGTTGC	180
AGCACTAGCG ATAGTCATCA TCAAGAAGAA GGTTGTTGCC ACGGGCATCA CGAG	234

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1035 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170

GGGGTTTTGA TTAGAACCCC CAAGCATTTA ACCAAGCAAG AGAGCGTGAA TTAGGGGCT	60
TACTACACGC CCCCTTATTT AGTGGATTGC GCTTACAAGC TTTTAAAAA GCATGTTGCT	120
ATTGAAAAC ACACGCTTTT AGACACCGCA TGTGGTAATA AAGAGTTTTT AAAGCTCCAC	180
CACCCTAAAA AAATAGGAGC GGATATTGAC CCTAAGTGTG ATGCTTTAAT AATAACGCT	240
CTAGCCAATC CTAAAAGAGA AAATTATGGC ATTAGCCAAG ATGAACCTTT AATCATCGTG	300
GGCAATCCCC CCTATAACGA TAGAACTTCC TTTATCAAAC AAGATATTAA AAATAAGAT	360
TTTATTTTTG AGATAGACAA CGATTTGAAA TCCCAGAGAT TAGGGATAAG TTTTTTAAAA	420
TCTTTTGCAA TTTTAAAGCC GCGGTTTATT TGCGTGCTAC ACCCTTTATC TTATCTCATC	480
AAAGAAGCTA ATTTTAAAGCA ATTAAAGCTA TTTAAGGATC ATTACAGGCT TTTAGACGCT	540
TTTGTTGTTT CTCTTAAATC TTTCACCTAA AGTAACGAAT TTCCTATTGT GATAGCTTTA	600
TATGAGCGAG GCGGAATGGA CTATGCAGGT ATTAGGCGTT TTGTTTTTCC AACTGATTGC	660
GATACGACGC TATGCTTAA CGATTTTGAC TACATAGCCA ATTATGTGGA TAAATACCCT	720
AACGCTAAAA AGGTTGGGCG ATCGGTGGGC TATTTTTTTC CTATGCGAGA CATTACGCT	780
CTCAAACGCA ACAAACCTTT TTTAAACGCG CCAAGCGAAA ATGCGGTGCG AATCAGTCAA	840
GATAAATTGA TTTATTACCA ATATATCCAT TATTTTAAGG AAATGCTCC TAAATCCCT	900
TATTATTTTG GTAATTGGA TATTATCATT GATCATTTTG CTTTTTTAGA AATTAAAGAC	960
GCTTTTTTAA AAGATAAAG AGCGCGTTTA GAATATTTTA AAAAATTGTT TCAAGGACAC	1020

SUBSTITUTE SHEET (RULE 26)

844

CCTTGTGAGT TTGAT

1035

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171

AATATTTTAA	AAAATTGTTT	CAAGGACACC	CTTGTGAGTT	TGATTAAAGT	TAGTGGTGAT	60
AAAAAAGTGA	TTGAGGTTTC	TATTCCTTTA	ACTTCCATTT	CAGGCAAAGC	GCGTGTGAAA	120
ATCAGACATG	CCTTTAGCGA	TTATGGTATT	TCAACAGCGA	CTAGAAAAAT	CCCTTTTAGT	180
TTAAAGCATT	ATGTAGAGTG	GCAGATCGGT	TATGATGTCC	CCATTAAAGA	TAAAGAAAAA	240
TTTGAACCTA	CTACTTTAAA	AGATGAAAAA	TATCATTTTT	TAGGGGCTAA	TAATAAAGTA	300
AAAACCTCTT	ATGAATTGAG	CGAAATGATT	TATTACGCTA	AGCGATTGGG	TTTAATCAGT	360
TTAGAAAATT	TAGAAAATAC	TTTAAAATTT	TTAGAAAAAC	AAAAACAATT	TATAGAAGAT	420
AATTTTATGA	TTACAAGAGA	AAGATTTAGA	TCGCATCAAT	TTGGTGGCAT	GGATTTTGAA	480
CTCTTACGCA	TTTCTTATCC	TTTGCTCATT	CATTCTTTTG	ATGATAATGA	GTTGAGCGAA	540
ATAGTTATTA	AGGAACAACA	ATATGGCTCT	AAAACCCAAG	CCATGCTGTA	TTTTTGCTTT	600
TCTATTTTGG	AGTTAAAAAC	CGCTACCCCC	TTATTAAACA	GAACCGCTAT	GCCCCAAGAA	660
CATGCCCTTT	TGATTATCCA	TGAAACCAAC	GCTCTTGTGT	TTTTAGAAAT	GCTTAAAATT	720
TTTGGACTTT	TAAGCCAAGT	GCACCATAAC	GATGTGTTAA	AGATTTTAGA	AAAAATACTT	780
CAAAAT						786

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172

SUBSTITUTE SHEET (RULE 26)

845

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TTGAAGGCAT TAAACGACTG CATGGTATTT TTTCATAAGA AAATTATTTT AAATTTTATC      60
TATTCCTTTAA TGGTTGCTTT TTTATTCCAT TTATCCTATG GGGTTCTTTT AAAAGCCGAT      120
GGAATGGCTA AAAAGCAAAC TCTTTTAGTG GGTGAAAGGC TTGTGTGGGA TAAGCTCACG      180
CTGTTAGGGT TTTTAGAAAA AAACCATATC CCCCAGAAAC TCTACTACAA TTTGAGCTCT      240
CAAGATAAAG AATTGAGTGC TGAATCCAA AGCAATGTTA CCTACTACAC TTTAAGAGAT      300
GCAATAACA CGCTCATTCA AGCCCTTATC CCTATTAGCC AGGATTTGCA AATCCATATT      360
TACAAAAAAG GAGAGGATTA TTTTITAGAC TTTATCCCCA TTGTTTTTAC TCGTAAAGAA      420
AGAACCCTCC TTCTTTCTTT ACAAACTTCG CCCTATCAAG ATATTGTCAA AGCCACCAAT      480
GACCCCTTT TAGCCAACCA ATTGATGAAC GCGTATAAAA AAAGCGTGCC TTTTAAACGC      540
CTAGTGAAAA ACGATAAAAT CGCTATCGTT TATACAAGGG ATTATCGTGT GGGGCAAGCG      600
TTTGGCCAGC CGACCATCAA AATGGCGATG GTTAGCTCTC GTTTCACCA ATACTATCTT      660
TTTTCCCAT CAAACGGGCG TTATTACGAT TCAAAAGCGC AAGAAGTGGC AGGGTTTTTA      720
CTAGAAACCC CGGTGAAATA CACCCGCATT TCTTCGCCTT TTTCGTATGG GAGGTTCCAT      780
CCTGTTTTTAA AAGTTAAACG GCCTCATTAC GCGGTGGATT ATGCGGCTAA ACATGGCAGT      840
TTGATCCATT CTGCTTCAGA CGGCCGTGTG GGTTTTATAG GGGTTAAGGC GGGTTATGGG      900
AAGGTGGTTG AAATCCATT GAATGAATTG CGCTTGGTGT ATGCTCACAT GAGCGCGTTC      960
GCTAACGGAT TAAAAAAGG CTCGTTCGTT AAAAAAGGGC AAATCATAGG AAGAGTGGGA      1020
AGCACGGGTT TAAGCACCAG GCCGCATTG CATTITGGCG TGTATAAAAA CTCCCGCCCC      1080
ATTAATCCTT TAGGCTATAT CCGCACCGCT AAAAGCAAGC TGCATGGCAA ACAAAGAGAG      1140
GTTTTTTTAG AAAAAGCTCA GTATTCTAAG CAAAATTAG AAGAACTTTT TAAAACCCAT      1200
TCTTTTGAAA AAAATTCATT TTATCTTTTA GAGGGTTTT      1239

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(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173

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GGATGCTTGA TGAAGAGCAT TTTGCTCTTT ATGATTTTTG TAGTTTGTC GTTAGAAGGC      60
AAAAAATTTT CACAAGATAA TTTTAAGGTG GATTATAACT ACTATTGCG CAAACAGGAT      120
TTGCACATCA TTAAGACGCA AAACGATTG TCCAATGCCT GGTATCTCCC TCCACAAAAA      180
GCCCCCAAAG AACATTCTTG GGTGGATTG GCTAAAAAAT ATTTAAACAT GATGGATTAT      240
CTAGGCACTT ATTTTGTGCC TTTTATCAT AGTTTCACCC CCATTTTTCA ATGGTACCAC      300
CCTAATATCA ACCCCTACCA ACGCAATGAG TTTAAGTTCC AAATCAGTTT TAGAGTGCCT      360
GTATTTAGGC ATATTCTTTG GACTAAAGGC ACGCTTTATC TGGCTTATAC CCAAATAAC      420
TGGTTTCAAA TTTATAATGA CCCTCAATCC GCCCCATGC GAATGATCAA TTTTCATGCCT      480
GAACTCATCT ATGTTTATCC TATTAATTT AAACCTTTTG GGGGTAAAAA AGGGAATTTT      540
TCTGAAATTT GGATAGGTTG GCAGCACATT TCTAATGGTG TGGGGGGTGC GCAATGTTAC      600
CAGCCTTTTA ATAAGAAGG TAATCCTGAA AACCAAGTTT CAGGACAACC TGTAATCGTT      660
AAAGATTATA ACGGGCAAAA AGATGTGCGC TGGGGGGGGT GTCGTTCCGT GAGCGCGGGC      720
AACGCCCTGT GTTTCGTTG GTGTGGGAAA AGGGAGGCC      759

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(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

SUBSTITUTE SHEET (RULE 26)

846

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174

ATGTGAAATT AAAGGGCATG GATAAAGAAG AAAATGAAGA AAATAAAATT AACCAAGCGA	60
ATGATAGCTA CGGCCAAAAA AGCCCTTTCC AAAAGCTATG GATATTGTTT GGTGGGGCGT	120
TTTTAATTT TCTTTTGGC GTTTGTAGTG ATTTTTTCT GGCATTGAGC GGGGAAAAAG	180
TCTTACTGCC CGTCATTGGC GGTTTAGAAA AAAACGCGCT AGAAGCCGGG CTGTAAAGG	240
GGGATAGAAT CTTCTATCA ACCATCAAAA AA	272

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175

AGAATTGAGT GGGGTAATAG GCATTGTGGG GCGTTAAGCC ATGCCAATAG CGTGAGCATG	60
CTTTTGTGT TTGGGGCGTT TTTATCTATC AATCTAGGGA TTTTAAATTT ATTACCCATT	120
CCAGCCTTAG ATGGGGCGCA AATGCTAGGG GTCGTTTTTA AAAATATTTT TCATATCGCT	180
TTGCCAACGC CCATACAAA TGCCTTGTGG CTAGTGGGGG TGGGGTTTTT GGTTTTGTG	240
ATGTTTTTAG GGCTTTTAA TGACATTACT CGTTTGCTA	279

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176

AATTTAGGCG	GAGCGGCCAA	TGTGGCTAAT	AACCTTACCT	CTTTAAAAGC	TAAAGTCTTT	60
TTATGTGGGG	TAGTGGGAGA	TGATTTAAAA	GGCAAGCATT	TCATTAGCAC	TTTAAATTCT	120
ATAAGGATTG	ACACTTCAGG	TGTTTTAATA	GATAAAACCC	GTTGCACCAC	GCTTAAAACG	180
CGCATCATCG	CGCAAAACCA	GCAAATCGTG	CGCGTGGATA	AGGAAATCAA	AGACCCCTTA	240
AACGCTGATT	TAAGAAAGAA	TCTTTTAGAT	TTTATCGCAG	AAAAAATTCA	AGAAATAGAT	300
GGCGTGATCC	TTTCAGATTA	CAATAAGGGT	GTGTTGGATT	TTGAACTCAC	TCAAACCATC	360
ATCACGCTAG	CTAATAAGCA	TCATAAGCTC	ATTTTATGCG	ACCCTAAAGG	AAAGGATTAT	420
AGCAAATATT	CCCATGCGAG	TTTGATCAGC	CCTAATCGCG	CTGAATTAGA	GCAAGCGCTC	480
CATTTGAAAT	TAGACAGCCA	TGCGAATTTA	TCAAAAGCGC	TCCAAATTTT	ACAAGAAACT	540
TATCATATCG	CTATGCCCTT	AGTAACCTTG	AGCGAACAAG	GCATCGCTTT	TTTAGAAAAA	600
GGCGAGTTAG	TCAATTGCCC	CACTATCGCT	AAAGAAGTTT	ATGATGTAAC	GGGGGCAGGC	660
GATACGGTGA	TAGCGTCTTT	AACGCTCTCT	TTATTGGAAT	CAAAAAGCTT	GAAAGAAGCT	720
TGCGAGTTTG	CTAATGCGGC	TGCGGCGGTG	GTGGTGGGTA	AAATGGGGAG	CGCGTTAGCG	780
AGTTTAGAAG	AAATCGCTTT	GATTTTGAAC	CAAACGCACC	CTAAAATCCT	CCCTTTAGAA	840
AAGCTGTTAG	AAACTTTAGA	ACGCAACCAG	CAAAAAATCG	TTTTCACCAA	TGGCTGTTTT	900
GATATTCTCC	ATAAAGGGCA	TGCGAGCTAT	TTGCAAAAGG	CTAAAGCTTT	AGGGGATATT	960
CTTGTTGTGG	GGTTAAATAG	CGATAATTCC	ATTAAAAGGC	TTAAGGGGGA	TAAACGCCCC	1020
ATAGTGAGCG	AAAAAGACAG	GGCGTTTCTT	TTAGCGAGCT	TGTCTTGCCT	GGATTATGTT	1080
GTGGTGTTTG	GAGAAGACAC	GCCCCATAAA	TGATTCAAG	CCCTAAAGCC	TGATATTTTA	1140
GTCAAGGGAG	CGGACTACCT	CAATAAAGAA	GTCATAGGGA	GCGAGTTGGC	TAAAGAAACC	1200
CGTTTGATAG	AATTTGAAGA	AGGTTATTCC	ACAAGCGCTA	TCATAGAAAA	AATTAAGG	1260
ACACATAATG	AT					1272

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 963 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177

GGATCGCTTA	TGGTGAATGT	GTTTTTCAAG	CAGCAAAAAT	TCGTCATTAA	AAAACGCTTT	60
AATGACTTTA	ATGGTTTTGA	TATAGAAGAA	AATGAAGTGT	TGTGGTTTGA	ATTAATCAAC	120
CCTACGCCCA	ATGAATTAGC	CACTCTAAGC	CAAGAATACG	CTATCCACTA	CAACACGGAT	180
CATTCCCAAC	GAGTCTCATC	AGTTACCAAA	TACTGGGAAG	ACAGCTCCAG	CGTTACGATC	240

SUBSTITUTE SHEET (RULE 26)

848

AACGCTTTTT	TCACCAACCA	GGATGAAAT	GAGACTTTC	ACATGGAAAT	GGCGACCTTT	300
ATTTTGTCTA	ATAACATTCT	TTTCACGATT	TATTACGGGA	CTTTAGAAAT	CTTTGATTCT	360
ATCCAAAAAA	AGGTTTGGC	TAGCCCTAAA	AAATTTGAAG	ACGGGTITGA	TATTCTAACT	420
AAAATCTTTG	AAGTGTATTT	TGAAAAAGGG	GTGGAATGTT	TGGAATGGAT	CAACAAACAA	480
ACGAGCCTGT	TGCGCAAAAA	CATCATTTTC	AAAGAAACTT	CTACGCATGA	TGATATTTTA	540
GTGCGCTTGT	CCAATTGCA	AGAATTTAAT	GTGGCTTTAA	GGGATTCCTT	TTTTGACAAA	600
CGGCGCATTA	TCACCGCTTT	ATTAAGGAGC	AATAAAGTGG	ATAGCGATAC	TAAAAATAAT	660
TTAAATATCA	TTTTAACCGA	TTTAGCTCT	TTGGTGGAGT	CTACAACGGT	CAATCTCAAC	720
TCGCTTGATA	ACATTCAAAA	CCTGTTCGCT	TCTCAAGTCA	ATGTGGAGCA	AAATAAAATC	780
ATTAAACTCT	TCACTGTGGC	GACTATGGCG	ATGATGCCCC	CCACATTGAT	TGGCACGATT	840
TATGGCATGA	ATTTTAAATT	CATGCCGGAG	TTAGAATGGC	AATACGGGTA	TCTTTTGGCG	900
CTGATTGTCA	TGGCGATTTC	TACGATTITG	CCGGTGATTT	ATTTCAAAAA	GAAGGGTTGG	960
TTG						963

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178

CCTTTCATGG	AATTTTTATC	CTCACTCTTA	GACGCTCTTT	CTACACCGCA	TGGCATAGTC	60
TCCTTGGCTA	CGCTCACGCT	TTTAGAGATC	GTTCTAGGGA	TTGATAATAT	CATTTTTATC	120
ACGGTGATGG	TTTATAAACT	CCCCAAACAC	CAGCAAAATA	AGGTCATGAT	TTTAGGCTTG	180
GGCTTAGCGA	TGATCACTCG	TATAGGGCTT	TTAGGGAGCT	TGTTTTTCAT	CAGCCATTTG	240
CAAAAGCCTT	TATTCGCTAT	AGCGGGCATG	AGCTTTTCAT	GGCGTGATGT	GGTGCTGCTT	300
TTAGGGGGGG	CGTTTTTGGC	TTTAAAGGCG	TTAGTGGGAAT	TAAAAGAGCA	GATCTATCCT	360
AAAGAAAAAC	GCCAAGAAAA	AGCGTTTGGC	TTTTTCATCA	CTTTAATAGA	AATCATGTTT	420
TTAGACATTG	TTTTTTCCTT	GGACTCCGTG	ATCACGGCTA	TTGGGATCGC	TAAACACTTA	480
GAAGTCATGG	CGCTTGCTAT	TATTTTATCT	GTAATCGTGA	TGATGTTTTT	TTCCAAAATC	540
GTTGGCGATT	TTATTGAAAA	GCATTATCGC	GTCAAAACTT	TAGCCTTTGT	GTTTTTGCTC	600
GTGTGGGGCG	TGTTTTTGTT	TTAGAAGGC	TTGCATTTAC	ACATCAATAA	AAACTATTTG	660
TATGCGGGTA	TTGGTTTTGC	CTTGCTCATA	GAATGCTTGA	ATATTTTCAT	AGAAAAGAAA	720
ATGAAAAAAA	GT					732

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

SUBSTITUTE SHEET (RULE 26)

849

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179

GTTTATGGCT	TTTGGGCTTG	TGTTTGTGC	TAGGGATTTA	AGTTTGGTTT	TGTTTATTTT	60
GCGCAAACAA	GGGCGTTTCA	ATTTAGACAA	AACCATTCTT	TCCATTAGCG	CTATCAATGA	120
AATGAGCATG	ATTTTAGGCC	TGTTTATGCT	CACAGCCGGG	AATTTCTTAG	GTGGGGTGTG	180
GGCGAATGAA	TCTTGGGGGC	GCTATTGGGG	GTGGGACCCT	AAAGAACTT	GGGCGTTGAT	240
TTCTATTTGC	GTCTATGCCT	TGATCTTGCA	TTTGCCTTTT	TAGGCTCTC	AAAATTGGCC	300
CTTTATTTTA	GCGAGCAGCA	GCGTGCTAGG	GTTTATTTCG	GTTTAAATGA	CTTATTTTGG	360
CGTGAATTAC	TACCTTTCTG	GCTTGCACAG	CTATGCCGCA	GGTGATCCTT	TGCCGATCCC	420
TACTTTTTTA	TACTTTTGG	TAGCGATACC	TTTCGCTCTC	GTATCTTGGC	GTATTTCAAA	480
CGCCATT						487

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180

CGATATTCCG	ATCAGACGAA	TCTATTAGCC	CTAAATGCTG	CTATTGAAGC	CGCAAGGGCC	60
GGCGAGCATG	GTAGAGGCTT	TGCGGTGGTG	GCTGATGAAG	TAGGAATTT	AGCTGGGCGC	120
ACTCAAAAGT	CTTAGCCGA	AATCAATTCC	ACTATCATGG	TGATTGTCCA	AGAAATCAAT	180
GATGTGAGTT	CGCAAATGAA	TCTCAATTCC	CAAAAAATGG	AGCGCTTGAG	CGATATGAGT	240
AAAAGCGTGC	AAGAACTTA	CGAAAAAATG	AGTTCTAATT	TAAGCTCAGT	CGTTTTAGAC	300
AGCAATCAAA	GCATGGACGA	TTACGCTAAA	TCCGGACACC	AAATTGAAGC	TATGGTAAGC	360
GATTTTGCAG	AAGTGAAAA	AGTGGCTTCT	AAGACTTTGG	CTGATTCTTC	AGATATTTTA	420
AACATCGCTA	CGCATGTGAG	TGGAACGACC	ATGAATTIAG	ACAAACAAGT	GAATTTGTTT	480
AAAACT						486

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

850

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181

ATTGTGTTAA AACTTAATCA GGGGGGAGTT TATCAAAAAA GGTTGGATT GTTAAAGGTT	60
TCTGTGATCA CGGCGTGTTT TAATAGCGAA AAAACCATTG AAGACACCAT TCTTTCCGTG	120
CTTAATCAAA CTTATAAAAA CATTGAATAC ATCATTATAG ATGGGGCTAG CGCGATAGCA	180
CTT	183

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1992 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182

AATCATATTG TCGTGGCGT TGATTGTGAT CGTGGCGTGA GCATTTTAGG GGTGTCCTTA	60
AACAGCAGGG TGAAAGAGAT TTTAAAAGAA AGCGCTCTGC ATTCAATGCA AGATAGTTTG	120
CATTTCAAGG TTAAGGAAGT GCAAAGTGTT TTGGAAAACA CTTATACGAG CATGGGCATT	180
GTCAAAGAAA TGCTCCCTGA AGACACCAAA AGAGAAATCA AAATCCAGTT GTTAAAAAAC	240
TTCAATTTAG CCAATTCGCA TGTCGCTGGG GTGAGCATGT TTTTAAAGA CAGAGAGGAT	300
TTGAGATTGA CGCTTTTACG AGATAACGAT ACGATCAAGT TGATGGAAA CCCGTCATTA	360
GGGAGTAACC CTTTAGTGCA AAAAGCGATG AAAAATAAAG AAATTTCTAA AAGCTTGCCT	420
TATTACAGGA AAATGCCTAA CGGGGCGGAA GTTTATGGCG TGGATATTCT TTTACCACTA	480
TTCAAGGAAA ACACGCAAGA AGTGGTGGGG GTTCTGATGA TTTTCTTTC CATTGACAGC	540
TTCAGTAATG AAATCACTAA AACAGGAGC GATTTATTTT TAATTGGCGT TAAAGGTAAA	600
GTGCTTTTGA GCGCGAATAA AAGCTTGCAA GACAAATCCA TCACCGAAAT TTATAAAAGC	660
GTGCCTAAAG CCACTAATGA AGTGATGGCT ATTTTAGAAA ATGGCTCTAA AGCGACTTTA	720
GAATACTTGG ATCCCTTTAG CCATAAGGAG AATTTTTTAG CCGTTGAAAC CTTTAAATG	780
CTAGGCAAAA CAGAAAGTAA AGACAATCTT AATTGGATGA TCGCTTTGAT CATTGAAAAA	840
GACAAGGTCT ATGAGCAAGT GGGATCGGTG CGTTTGTGG TGGTTGCAGC GAGTGCTATC	900
ATGGTGTTAG CCTAATCAT AGCGATCACT CTTTAAATGC GAGCGATCGT GAGCAATCGT	960
TTGGAAGTCG TTTCTAGCAC CTTGTCTCAT TTCTTTAAAT TATTGAACAA TCAAGCCCAT	1020
TCTAGCGACA TTAAATTGGT TGAAGCGCGA TCTAATGACG AATTAGGGCG CATGCAAACA	1080
GCGATCAATA AAAATATCTT GCAAACCCAA AAAACCATGC AAGAAGACTG GCAAGCCGTC	1140
CAAGACACCA TTAAGTGGT TTCAGATGTG AAAGCGGGGA ATTTTGCAGT GCGCATCAGC	1200
GCTGAACCCG CAAGCCCTGA TTTGAAAGAA TTGAGAGACG CGCTAATGGA TCATGCACTA	1260
TTTGCAAGAA AGCGTGGGAC TCACATGCCA AGCATTTTCA AAATCTTTGA AAGCTATTCT	1320

SUBSTITUTE SHEET (RULE 26)

851

GGCTTGATT	TTAGAGGGCG	GATCCAAAAC	GCTTCGGGTA	GGGTGGAATT	GGTTACTAAC	1380
GCTTTAGGGC	AAGAAATCCA	AAAAATGCTA	GAAACTTCGT	CTAATTTTGC	CAAAGATCTA	1440
GCGAACGATA	GCGCGAATTT	AAAAGAATGC	GTGCAAAATT	TAGAAAAGGC	TTCAAACCTC	1500
CAACACAAAA	GCCTGATGGA	AACTTCCAAA	ACGATAGAAA	ATATCACCAC	TTCCATTCAA	1560
GGCGTGAGCT	CTCAAAGTGA	AGCCATGATT	GAACAAGGGA	AAGACATTAA	AAGCATTGTA	1620
GAAATCATT	GAGATATTGC	CGATCAAACG	AATCTATTAG	CCCTAAACGC	TGCTATTGAA	1680
GCCGCACGAG	CCGGCGAGCA	TGGCAGAGGC	TTTGGCGTGG	TGGCTGATGA	GGTGAGGAAG	1740
CTCGCTGAAA	GGACGCAAAA	ATCCCTCAGT	GAGATTGAAG	CCAATATTAA	TATTCTCGTT	1800
CAAAGCATT	CAGACACGAG	CGAAAGCATT	AAAAACCAGG	TTAAAGAAGT	AGAAGAGATC	1860
AACGCTTCTA	TTGAAGCCTT	AAGATCGGTT	ACTGAGGGCA	ATCTAAAAAT	CGCTAGCGAT	1920
TCTTTAGAAA	TCAGTCAAGA	AATTGACAAA	GTCTCTAACG	ATATTTTAGA	AGATGTGAAT	1980
AAAAAGCAGT	TT					1992

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183

CGTGGTGAAT	GCTATTTTGA	AAGAGAAATT	GGATTGATGA	GGAAAATTTT	TTCTTATATT	60
TCTAAGGTC	TATTATTTAT	TGGGGTGGTT	TATGCAGAGC	CTGATTCTAA	AGTGAAGGCC	120
TTAGAAGGGA	GGAGCAAGA	GTCTTCTTTG	GATAAAAAAA	TCCGCCAAGA	ATTGAAGAGT	180
AAGGAATTGA	AGAATAAGGA	ATTAAAGAAT	AAGGATTTGA	AAAATAAAGA	AGAAAAGAAA	240
GAAACAAAAG	CCAAGAGAAA	ACCCAGAGCA	GAAGTCCATC	ATGGGGACGC	CAAAAAATCCC	300
ACTCCAAAGA	TCACGCCTCC	TAAATCAAAA	GGGAGTAGTA	AGGGCGTTCA	AAATCAAGGC	360
GTTCAAAACA	ACGCGCCAAA	ACCTGAAGAA	AAAGATACAA	CCCCTCAAGC	TACTGAAAAA	420
AATAAGGAAA	CAAGCCCTAG	CTCTCAATTC	AATTCCATTT	TTGGTAATCC	TAATAACGCT	480
ACCAACAACA	CCCTTGAAGA	TAAGGTCGTA	GGGGGCATTT	CATTGCTTGT	TAATGGTTCTG	540
CCTATCACGC	TGTATCAAAT	CCAAGAAGAG	CAAGAAAAAT	CTAAAGTGAG	TAAGGCTCAA	600
GCTAGGGATC	GTTTGATCGC	TGAACGCATT	AAAAACCAAG	AAATTGAGCG	CTTAAAAATC	660
CATGTAGATG	ATGACAAGCT	AAACCAAGAA	ATGGCGATGA	TGGCGCAACA	ACAAGGCATG	720
GATTTAGACC	ATTTCAAACA	GATGCTTATG	GCTGAGGGGC	ATTATAAACT	CTATAGAGAT	780
CAACTTAAAG	AGCATTTAGA	AATGCAAGAA	TTGTTGCGTA	ATATTTTGCT	CACGAATGTG	840
GATACCAGCT	CTGAAACCAA	AATGCGCGAA	TATTACAACA	AACACAAGGA	GCAATTCACT	900
ATCCCCACAG	AAATAGAAAC	CGTGCGCTAC	ACTTCCACCA	ATCAAGAGGA	TTTAGAAAGG	960
GCTATGGCAG	ACCCTAATTT	GGAAGTCCCA	GGGGTGAGTA	AGGCCAATGA	AAAAATAGAG	1020
ATGAAAACCC	TAAACCTCA	AATCGCCCAA	GTCTTTATTT	CGCATGAGCA	AGGCTCTTTC	1080
ACGCCCGTTA	TGAATGGGGG	TGGGGGGCAG	TTCATCACCT	TTTATATCAA	GGAAAAAAGG	1140
GGTAAAAATG	AAGTGAGCTT	CAGTCAGGCC	AAGCAATTCA	TCGCCCAAAA	ATTAGTGGAA	1200
GAATCTAAGG	ATAAGATTTT	AGAAGAGCAT	TTTGAAAAAT	TGCGCGTTAA	GTCTAGGATT	1260
GTGATGATCA	GAGAG					1275

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs

SUBSTITUTE SHEET (RULE 26)

852

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1008
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184

ATTGTGCAAC	ACTTCAATTT	CCTCTATAAA	GATTCTTTAT	TTTCTATCGC	TTTATTCACT	60
TTCATTATCG	CTCTTGTGAT	TTTATTAGAA	CAGGCTAGAG	CGTATTTTAC	CCGAAAGAGA	120
AACAAAAAAT	TTTTGCAAAA	ATTCGCCCAA	AATCAAAACG	CCTATGCGAG	CAGCGAGAAT	180
TTAGACGAGC	TTTTAAAGCA	TGCTAAAATT	TCCAGTTTGA	TGTTTTTAGC	TAGGGCGTAT	240
TCTAAAGCGG	ATGTGGAAAT	GAGCATTGAA	ATCTTAAAG	GGCTTTTGAA	TCGCCCCCTTA	300
AAAGATGAAG	AAAAAATCGC	TGTTTTAGAT	TTATTGGCTA	AAAATTATTT	TAGCGTGCGG	360
TATTTGCAGA	AAACAAAAGA	CACCGTGAAA	GAAATTTTGC	GCTTTTCCCC	AAGGAATGTG	420
GAAGCGTTGT	TGAAGCTTTT	GCATGCGTAT	GAATTAGAAA	AAGATTATTC	AAAGGCTTTA	480
GAAACTTTGG	AATGTTTGGA	AGAATTAGAG	GTGCCATAAA	TTGAAACGAT	TAAAAATTAC	540
CTCTATTTA	TGCATTTAAT	AGAGAATAAG	GAAGATGCGG	CTAAAATCTT	GCATGTTTCA	600
AAAGCGTCGT	TAGATTTGAA	AAAAATCGCT	CTGAATCACT	TAAAATCGCA	TGATGAAAAT	660
CTTTTTTGGC	AAGAAATTGA	TACAACCGAA	CGGCTAGAAA	ATGTGATCGA	TCTTTTATGG	720
GATATGAATA	TCCCTGCTTT	TATTTTAGAA	AAACATGCCC	TTTTGCAGGA	CATCGCGCGA	780
TCTCAAGGGT	TGCTTTTGGA	TCACAAACCT	TGCCAAATTT	TTGAATTAGA	GGTTTTACGC	840
GCTCTATTGC	ATAGCCCTAT	AAAAGCGAGT	CTGACTTTTG	AATACCGCTG	CAAGCATTGC	900
AAACAAATCT	TTCTTTTGA	AAGCCATAGG	TGTCCTGTGT	GTTACCAGTT	AGCGTTTATG	960
GATATGGTGC	TTAAAATCTC	TAAAAAACG	CATGCTATGG	GAGTGGAT		1008

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185

ATTAGAGGCG	CAAAAACGGG	TCAAAACGAC	CACCTAAAGG	GAAAAATGAT	GAAAAACAAA	60
CGCTCTCAAA	ATAGCCCTTA	TGTAACGCCT	GACAACCCCT	ATCTAACGCT	AGAAAAAGCT	120
TTAGGGTATT	CTTTTAAAGA	CAAGCGTTTA	TTGGAGCAAG	CCTTAACGCA	TAAATCATGT	180
AAGCTCGCTT	TAAACAATGA	GCGCTTGGA	TTTTTGGCG	ATGCGGTGTT	GGGCTTGGT	240

SUBSTITUTE SHEET (RULE 26)

853

ATAGGGGAGC	TGCTATACCA	TAAATTCTAT	CAATACGATG	AGGGCAAAC	CTCTAAATTA	300
AGGGCTTCTA	TTGTGAGCGC	GCATGGTTTC	ACTAAATTAG	CGAAAGCGAT	TGCTTTACAA	360
GATTATTTGC	GCGTTTCTTC	TTCTGAAGAA	ATTCTAAGG	GGAGGGAAAA	ACCCTCTATT	420
CTGTCAAGCG	CTTTTGAGGC	TTTAATGGCT	GGGGTGTATT	TAGAAGCAGG	GTTAGCTAAG	480
GTGCGTAAAA	TCATACAAAA	TTTACTCAAT	CGTGCTTACA	AGCGTTTGA	TTTGGAGCAT	540
TTGTTTATGG	ATTATAAAAC	CGCTTTGCAG	GAATTGACCC	AAGCGCAGTT	TTGCGTGATC	600
CCCACCTTACC	AATTACTCCA	AGAAAAAGGC	CCCGATCACC	ATAAAGAATT	TGAAATGGCT	660
CTATACATTC	AAGATAAAAT	GTATGCGACC	GCTAAAGGCA	AGAGTAAAAA	AGAAGCCGAA	720
CAGCAATGCG	CTTATCAAGC	GCTTCAAAAA	CTTAAGGAAG	TCAA		765

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186

GCGCATCAAT	CATCTCGTGG	TGTTAGCATG	ATTTTAGCAT	GCGATGTGGG	GTAAAAACGC	60
ATTGGAATCG	CTGCGCTTTT	AAACGGCGTT	ATCTTGCCTT	TGGAAGCGAT	TTTACGCCAC	120
AACAGGAATC	AAGCCTCTAG	GGATTGTAGC	GATTTATTGA	GAAGAAAAAG	CATTCAAGTG	180
CTGGTGGTGG	GCAAAACCAA	CGAAAGCTAT	GCAGATACCC	ACGCCCCGAT	TGAGCATTTT	240
ATCAAGCTTG	TAGATTTTAA	GGGCGAAATC	GTTTTTATCA	ATGAAGATAA	TTCTAGCGTA	300
GAAGCTTATG	AAAATTTAGA	GCATTTGGGT	AAGAAAAATA	AGCGGATCGC	TACCAAAGAT	360
GGCCGTTAG	ACTCTTTGAG	CGCTTGTAGG	ATTTTAGAGC	GCTATTGCCA	GCAGGTTTTA	420
AAAAAGGGC						429

(2) INFORMATION FOR SEQ ID NO:1187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1731

SUBSTITUTE SHEET (RULE 26)

854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187

AAGAATGAAA	ATTTTATCAA	GGTTTTAATA	TTGGATTATA	AGGTATTATT	GCAACGGATT	60
GTTGATTTTT	TCATCAAGCT	CAATAAAAAG	CAAAAAATCG	CCCTGATCGC	AGCGGGGGTT	120
TTGATCACCG	CTTTACTCGT	GTTTTTATTG	CTCTATCCTT	TTAAAGAAAA	AGACTACGCG	180
CAAGGGGGTT	ATGGGGTTTT	ATTTGAAAGA	TTGGATTCTA	GCGATAACGC	CTTAATCTTA	240
CAACACCTCC	AGCAAAAACCA	AATCCCTTAT	AAAGTCTTAA	AAGACGACAC	CATTCTTGTC	300
CCTAAAGATA	AAGTGTATGA	AGAAAGGATC	ACTCTGGCTT	CTCAAGGGAT	CCCTAAAACG	360
AGTAAAGTGG	GCTTTGAAAT	CTTTGACACT	AAAGACTTTG	GGGCGACTGA	TTTTGATCAA	420
AACATCAAAC	TCATTGCGCG	CATTGAGGGG	GAATTGTGCG	GCACGATTGA	AAGTTTAAAC	480
CCCATTCTTA	AAGCCAATGT	GCATATTGCA	ATCCCTAAAG	ACAGCGTGTT	TGTGGCTAAA	540
GAAGTCCCTC	CTAGCGCTTC	AGTGATGCTC	AAGCTTAAGC	CTGACATGAA	GCTTTCACCC	600
ACTCAAATTT	TAGGGATTAA	AAATTTAATC	GCTGCAGCTG	TGCCTAAACT	CACGATAGAA	660
AACGTGAAAA	TCGTGAATGA	AAATGGCGAA	TCAATAGGCG	AGGGCGATAT	ACTAGAAAAC	720
TCCAAAGAAT	TAGCCTTAGA	GCAATTGCGC	TACAAACAAA	ATTTTGAAAA	CATTTTAGAA	780
AATAAGATCG	TCAATATCTT	AGCCCTTATT	GTGGGGGGTA	AAAACAAGGT	GGTCGCAAGG	840
GTCAATGCGG	AGTTTGATTT	CAGCCAAAAG	AAAAGCACCA	AAGAGACTTT	TGATCCCAAT	900
AATGTCGTAA	GGAGCGAGCA	AAATTTAGAA	GAAAAAAAAG	AAGGCGCTCC	TAAAAAACAA	960
GTGGCGGTG	TGCCGGGAGT	TGTGAGCAAT	ATTGGGCCTG	TGCAAGGATT	GAAGGACAAT	1020
AAAGAGCCAG	AAAAATACGA	AAAGTCTCAA	AACACGACCA	ATTATGAAGT	GGGTAAAACC	1080
ATTATCGAGA	TCAAGGGCGA	GTTTGGCACC	TTAATGCGTT	TGAATGCGGC	GGTTGTGGTG	1140
GATGGCAAAGT	ATAAAATCGC	GCTCGAAGAC	GGGGCAAACG	CTTTAGAATA	CGAGCCTTTA	1200
AGCGATGAAT	CGCTTAAAAA	AATCAACGCC	CTAGTCAAAC	AAGCCATTGG	TGATAATCAA	1260
AATAGAGGCG	ATGATGTGCG	GGTGAGTAAT	TTTGAGTTTA	ACCCTATGGC	GCCTATGATT	1320
GACAACGCCA	CTTTGAGCGA	AAAAATCATG	CATAAACTC	AAAAATCTT	AGGCTCATTT	1380
ACGCCCTTAA	TCAAGTATAT	TTTGGTGTTC	ATAGTGTTAT	TCATTTTCTA	TAAAAAAGTG	1440
ATCGTGCCTT	TCAGCGAACG	CATGCTGGAA	GTGGTGCTTG	ATGAAGATAA	GGAAGTGAAA	1500
TCCATGTTTG	AAGAAATGGA	CGAAGAAGAA	GATGAGTTGA	ACAACTCGG	CGATTGAGG	1560
AAAAAAGTAG	AAGATCAATT	AGGGCTTAAT	GCAAGCTTTA	GCGAAGAAGA	AGTAAGATAT	1620
GAAATTATTT	TAGAAAAGAT	TAGAGGAACC	CTTAAAGAGC	GTCCTGATGA	AATCGCCACG	1680
CTCTTTAAAC	TCTTAATCAA	AGATGAAATC	TCTTCAGACA	GCGCGAAAGG	T	1731

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188

AAATGGTGGC	GTTATTGTGA	GCGGAGGAGC	GTTAGGCGTG	GATATTATCG	CTCAAGAAAA	60
CGCCTTACCA	AAAACCATCA	TGCTTTTCGCT	TGCAGTTTGG	ATTTTATCTA	TCCCACGAAC	120
AACCATAAAG	TGATCCAAGA	AATCGCGCAA	AACGGTTTGA	TTTTAAGCGA	ACATGAAAAG	180
GATTTTCATGT	TTATTAAAGG	TTTTTTTTTA	GTTAGAAATT	GTCTGGTGAT	CGCTTTAACC	240
GACCGGGTGA	TTATCCCCCA	AGCGGATTTA	AAAAGCGGCT	CTATGAGTAG	TGTGAGATTA	300
GCCAGAAAT	ACCAAAAACC	CTTGTTTGTT	TTACCCCAAC	GCCTGAATGA	GAGCGACGGC	360
ACTAATGAGC	TTTTAGAAAA	AGGGCAGGCT	CAAGGGATAT	TTAATATTCA	AAATTTTATA	420
AACACCTTTT	TAAAGATTA	CCATTAAAAA	GAAATGCCTG	AAATGAAAGA	TGAATTTTAA	480
GAATATTGCG	CGAAAAACCC	TAGCTATGAA	GAAGCGTATC	TCAAATTTGG	GGATAAGCTT	540

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TTAGAATACG AGCTGTTGGG TAAGATTAAG CGCATCAATC ATCTCGTGGT GTTAGCA

597

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189

AGGTTAAAAA	TGGCAACCAA	GCTTACCCCC	AAACAAAAGG	CTCAATTAGA	CGAACTTTCC	60
ATGAGTGAAA	AAATCGCCAT	TTTACTCATT	CAAGTGGGCG	AAGACACCAC	AGGCGAGATT	120
TTAAGGCATT	TAGACATTGA	CTCTATTACA	GAGATTTCTA	AGCAAATCGT	GCAATTAAAC	180
GGCACGGACA	AGCAAATCGG	CGCGGCGGTT	TTAGAGGAAT	TTTTTGCGAT	CTTTCAGTCT	240
AACCAATACA	TCAATACCGG	CGGTTTAGAA	TACGCTAGGG	AGCTTTTAAAC	CAGGACTTTA	300
GGGAGCGAAG	AAGCCAGGAA	AGTGATGGAC	AAACTCACTA	AAAGCTTGCA	AACGCAAAAA	360
AACCTCGCTT	ATTTAGGCAA	AATCAAGCCC	CAACAACTCG	CTGATTTTCAT	CATTAAACGAA	420
CACCCTCAAA	CCATCGCCTT	GATTTTGGCC	CACATGGAAG	CCCCTAATGC	GGCTGAAACT	480
TTGAGCTATT	TCCCTGATGA	AATGAAAGCC	GAGATTTCCA	TTAGAATGGC	GAATTTAGGC	540
GAAATATCGC	CCCAAGTGGT	TAAAAGGGTT	TCCACGGTGT	TAGAAAACAA	ACTAGAATCG	600
CTCACTAGCT	ATAAAATTGA	AGTGGGCGGC	TTGAGAGCGG	TGGCTGAAAT	CTTTAACCGC	660
TTGGGCCAAA	AGAGTGCCAA	AACCACGCTC	GCTCGCATTG	AAAGCGTGGA	TAACAAACTC	720
GCCGCGCGCA	TTAAAGAAAT	GATGTTCACT	TTTGAAGATA	TAGCCAAACT	AGACAATTTT	780
GCTATCATGA	GAGATTTTAA	AAGTGGGGGA	TTAAAAAAGA	CTGGTCTT		828

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190

SUBSTITUTE SHEET (RULE 26)

856

AGAAGTTTGG	GAAAAGGGCG	ACCAATGAAC	AAGAAAAATA	GCGTAATTTT	TGGTTTGATG	60
AATTTTTTTA	GCGAAAAGAA	TGAGCGCTGG	CTGTTAGCCC	ACAGGCACAC	GAGGGGGTTT	120
GTGATAGTGG	CGTGGCTTTT	TAGGTTTAAA	AGCATTGCGT	TTTCTATTTT	AATCACTCTG	180
TTGGTTATTT	TAGTGGATAT	TTGGGTGTAT	AGCGATGTGC	GCCAGTTTTT	ATTGGACACT	240
TCTAGCTCTT	TTATTTGGCT	TTTAATCGCT	TTACTAATCA	AGTGGGGCGT	GATTGTTATA	300
AGTGCGCGCA	AATGCTACCA	ATTGAGCCAA	AAAATGTTTG	CGTTAATCCA	AAGAAAAAGG	360
CAAATCAGAG	AGAATTTAAA	AAACCGCTCC	AATCGCAAAG	ATGCTAAAAA	TTTTGAAAAA	420
CTCTCTAACA	TCGCTGAAGA	AATCATTTCA	AAAAACAAG	AAGAGTCCCA	CCACAAAGAA	480
GATTCTAATG	ATGAAAACCA	CAAAGACAAG	CTTTCTAACA	TTACCGAAGA	AATGATTCTC	540
AAAAACAAG	AGGAACTGAA	AGCTAGAAAG	GATAAGGGGG	AT		582

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191

CTTATGGATA	GAGCCAAATT	TATATTCGTT	ACAGGGGGCG	TGTTAAGCTC	TCTAGGGAAA	60
GGGATTTTCAT	CTTCTTCAAT	CGCTACGCTT	TGCGAGCATT	GCAATTACCA	GGTTTCTATT	120
TTGAAGATTG	ATCCTTATAT	CAATATTGAT	CCAGGCACCA	TGAGCCCTTT	AGAGCATGGG	180
GAAGTGTTTG	TTACTAGCGA	TGGCGCTGAA	ACGGATTTAG	ACATCGGGCA	TTATGAACGC	240
TTTTTGAACA	GGAATTTAAC	GAGGTTGAAT	AATTTCACTA	CCGGGCAGAT	TTTTTCAAGC	300
GTGATAGAAA	ATGAAAGGAA	AGGGGAATAT	TTAGGCAAAA	CCATTCAAAAT	CGTCCCCCAT	360
GTAACCGATG	AAATCAAAAG	GCGCATTAAA	AGTGCGGCTA	AGGGGTTGGA	TTTTTTAATC	420
GTGGAAGTGG	GTGGAACCGT	GGGCGATATG	GAGGGCATGT	TTTATGTGGA	ACCGATCCGC	480
CAGCTGAAAC	TGGAATTACG	GAATAAAGCA	CTCATCAATA	TGCATGTAAC	CTTGATGCCC	540
TATATCCCGT	CCACTAGCGA	ACTAAGAAGC	AGACCCACGC	AACACTCCGT	CCAGGAATTA	600
CGGCGTCTTG	GCGTAACCCC	TCAAATCATT	TTGGCGCGAT	CGCCTAAGCC	TTTGATATAA	660
GAATTGAAAA	AGAAAATCGC	TTTGAGTTGC	GATGTGGAAC	AAGACAGCGT	GATTGTAGCC	720
ACAGACACTA	AAAGCATTTA	CGCATGCCCT	ATTCTTTTCT	TGCAAGAAGG	CATTTTAACC	780
CCCATTGCCA	GACGCTTTAA	TTTGAATAAG	TGCGACCCTA	AAATGGCGGC	TTGGAACACT	840
TTAGTAGAAA	AAATCATCGC	TCCTAAACAC	AAGGTCAAAA	TTGGTTTTGT	GGGCAAGTAT	900
TTAAGCTTAA	AAGAATCTTA	TAAATCCTTG	ATTGAAGCCC	TAATCCATGC	GGGGGCGCAT	960
CTGGATACGC	AAGTCAATAT	TGAATGGCTG	GATAGCGAGA	ATTTTAAATGA	AAAGACTGAT	1020
TTAGAGGGCG	TTGATGCGAT	TTTAGTGCCG	GGGGGCTTTG	GAGAAAGGGG	GATTGAGGGC	1080
AAAATTTGCG	CCATTCAAAG	GGCTAGGTTA	GAAAACTCC	CCTTTTTAGG	GATTTGTTTG	1140
GGCATGCAAT	TAGCGATCGT	TGAATTTTGT	CGCAATGTTT	TAGGCTTGAA	AGGGGCTAAC	1200
TCTACGGAAT	TTAACCAACG	CTGCGAATAC	CCTGTGGTGT	ATTTGATTGA	AGATTTTATG	1260
GATCAAAACC	ACCAAAAACA	GGTGCGCACC	TATAATTGCG	CTTTAGGAGG	CACCATGCGA	1320
TTAGGCGAAT	ACGAATGCGA	AATCATGCCT	AATAGCTTGC	TAGAAAAAGC	CTATAAAAAG	1380
CCTAATATCA	AAGAAAGACA	CGCCATCGT	TATGAAATCA	ACCCCAAATA	CCGCCAAGAG	1440
TGGGAAAATA	AAGGCTTGAA	AGTGGTGGGC	TTTGGGGCGA	ATCATTTTGT	TGAAGCGATT	1500
GAATTAGAAG	ATCACCCTTT	CTTTGTGGGG	GTGCAATTCC	ACCCGGAATT	CACCTCCAGG	1560
TTGCAAAGCC	CTAACCTTAT	TATTTTGGAT	TTCATTAAAG	GCGCTCTTCA	TAAATCC	1617

(2) INFORMATION FOR SEQ ID NO:1192:

SUBSTITUTE SHEET (RULE 26)

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192

ATATGGCGTG	GATGTGGAAG	CCATGACAGG	GTGCATGATG	AGTTTGTTTT	TGCTCGTTAC	60
ACGAAGGCTA	ATTACGAAAA	CACTTATTAC	GATACAGAGT	TTTCGCATTT	AAAAGAAGCG	120
AGCGCGTATT	TTCCGGACAT	TGATGAAGCG	AGCCTTTTTA	CGGATTTGCA	AGATTATTTT	180
AACTCATGGA	AAGAATTGTC	TAAAAACGCC	AAAGACTCCG	CTCAAAAACA	GGCTCTCGCT	240
CAAAAAACAG	AAGCTTTAAC	GCACAACATT	AAAGACACCA	GAGAGAGGTT	AACGACCTTA	300
CAGCATAAAG	CGAGCGAAGA	ATTAAAAAGC	GTCATTAAAG	AAGTCAATAG	CCTGGGTTCT	360
CAATCGCTG	AGATCAACAA	ACGCATTAAA	GAAGTGGAAA	ACAACAAGAG	TTTAAAGCAT	420
GCGAATGAGT	TAAGGGATAA	GCGAGATGAA	TTAGAGTTTC	ATTGCGGAGA	GCTTTTAGGG	480
GGGAATGTTT	TTAAAAGCAG	CATTAAAACC	CATTGCTCA	CAGATAAAGA	CTCAGCGGAC	540
TTTGATGAGA	GCTATAACCT	TAATATCGGG	CATGGGTTCA	ATATCATTGA	TGGCTCTATT	600
TTCCATCCCT	TAGTGGTTAA	AGAATCCGAA	AATAAAGGGG	GTTTGAACCA	GGTTTATTTT	660
CAAAGCGATG	ATTTTAAGCT	CACTAATATT	ACCGACAAGC	TCAATCAAGG	GAAAGTGGGG	720
GCGTTATTGA	ATGTGTATAA	TGACGGCTCT	AACGGGACTT	TAAAGGGCAA	GTTGCAAGAT	780
TATATTGATT	TGTTGGATTG	TTTTGCTAGG	GGCTTGATAG	AATCCACGAA	TGCGATTTAC	840
GCTCAAAGCG	CGAGCCATCA	TATTGAGGGC	GAGCCTGTGG	AGTTTAATAG	CGATGAAGCC	900
TTTAAAGACA	CGAATTACAA	TATCAAAAAC	GGCTCGTTTG	ATTTAATCGC	TTACAACACC	960
GATGGTAAAG	AAATCGCCAG	GAAAACCATT	GCTATCACGC	CCATTACAAC	CATGAACGAC	1020
ATTATCCAAG	TCATTAACGC	TAACACCGAT	GACAATCAAG	ACAACAACAC	CGAAAACGAT	1080
TTTGATGAAT	TATTTACAG	CGAGCTT				1107

(2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193

SUBSTITUTE SHEET (RULE 26)

858

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AAAACAAAGC TCGTTTTTAT GATAAAAGCG CGGTTTAAAA AACGCCTTTT AGGATCTAGG      60
GGCGCGTTTG ATTTGAATAT AGACTTAGAA ATTAAAGAAG CAGAAGTTGT CGCTTTATTA      120
GGAGAATCGG GAGCGGGTAA AAGCACGATC TTACGCATTT TAGCAGGGCT TGAAGCGGTG      180
AGTAGCGGCT ATATTGAAGC CAATCATTCA GTATGGTTAG AACTCAAAA AAAGATTTTT      240
TTAAAACAC AACAGCGAAA AATCGGCTTT GTGTTTCAAG ATTACGCCCT ATTCCCTCAT      300
TTAAACGTGT ATCAAACAT CGCCTTTGCT CACCCTAAAG ATAAAAATAA AATCCACGAA      360
GTGTTACGCT TAATGCGTTT AGAAAACCTA AGCCAGCAAA AAATTCCCAA ACTCTCTGGC      420
GGGCAAGCCC AACGAGTCGC TTTAGCAAGA GCTTTAATCG CAGCCAAAAA TCTATTGCTT      480
TTAGATGAGC CTTTAAACGC CCTAGATAAC GCCTTAAAAA ACGAGGTGCA ACAAGGTTTG      540
CTTGATTTTA TCAAGCGTGA AAATTTAAGC GTGTTATTGG TAAGTCATGA TCCAAACGAA      600
ATAACCAAC TCGCGCGAAC TTTCTCTTT TTAACAATG GCGTTATTGA TCCTAATCAA      660
GAAAATCGGC TTTTTCAAA CCGCTTATG GTAAACCTC TCTTTGAAGA TGAAAATTAT      720
TGCCATTATG AGGTCATTCC TCAAACGATC AGTTTGCCCA AAGATTGTCT GAACCCAACT      780
TTAAGCTTG ATTTCAATCA AAACAAAAA TTT                                     813

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(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194

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GGCTTATCCG CTACTATTCT TGGTATGTGG ATTATGTCTT CACTTCTAG TTCATTCTTT      60
CATTCGCTCT TCTTCATCAA ATCAAACCTT GGCCAACTCT TAAAAGGTTG GGGTTCAAAA      120
ATCTTTTTC TAAATAGAAA GTTTGTTTTA GCACAGTATA ATCCTAGCGT TTCAATTTTT      180
ATTTTACTCA ATAGGGTGTT TGGTGTGGC GTT                                     213

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(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

859

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195

ATTACAGCGCT CGCACCAGCT CTTTAATTTG CAAGAAAAAA AAGGGATTCT TGGTTTTTTA	60
CACCAAAAAA ATATCTTAAA TATTGCTCAA AATGACATCC ACCAGCTCCT TATTCTCATG	120
GTGGTCTTTT CTATGTTAGC AACCCCTTTT ATTTTAAAT ACCTAGAATC TATCGCTCAA	180
TTTATTTTGC ACCAAAAGAG CCAAGAAAAC GAGCCGGCTA AAAAA	225

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196

GGCTTGATGC GCATTATCAT AAGGTTACTT TCATTAAAA TGAACGCTTT TTTAAAACTC	60
GCGCTCGCTT CTTTGATGGG GGGGCTTTGG TATGCTTTCA ATGGCGAAGG CTCTGAGATT	120
GTCGCTATAG GGATTTTTGT GTTGATCTTG TTGTTTTT TTATCCGCCC TGTGAGTTTC	180
CAAGACCCAG AAAAACGAGA AGAATACATA GAACGGCTTA AAAAAACCA TGAGAGGAAA	240
ATGATCTTAC AAGACAAGCA AAAAGAAGAG CAAATGCGCC TCTATCAAGC CAAAAAAGAG	300
CGAGAGAGCA GGCAAAAACA AGACCTTAAA GAACAAATGA AAAAATACTC A	351

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197

AGGAAAAAAA TGGAAATCAT TTTATTAATT GTTGC GGCGG TTGTGTTGTT TTATTTTAC	60
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SUBSTITUTE SHEET (RULE 26)

860

AACACCCTCA	AAGAATATTT	GAAAAACCCC	CTAAACCCTA	AAACCAAAAC	CGAAGAATAC	120
GACTTGAAAA	ATGACCCCTA	TTTGCTGGTG	CAATCTAGCC	CCCTAGACAA	ATTCAAGCAA	180
ACCCAAATAG	GCGCGTATAT	GCGTCTTTTA	AAATTTTATG	ACATTCAAAA	AAACGCCTTG	240
GATAACGCTT	TAAGAACGCT	TTTATCCAT	GAATTGGAGC	AGCCCTTAAA	CAGCGAACAG	300
CAAAATTTAG	GCCAAAGAGC	TTCTCAA				327

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198

ATGCCTAATA	ACGCTTTATT	GCAAATCAAA	CAAGACACCC	TAAGTCTCAT	TGACGATTTA	60
AAAGTCATTT	GCAAGGATGC	TGGTTTAGCG	GGCGACGGCA	ACGGATACAA	GATCATCACG	120
CAATGCTTTT	TGTATAAATT	CTTATGCGAT	AAGTTTGAAT	TCTTTTTTGA	ACAAAAATTC	180
CCCAACAAAA	CGATACGAGA	CTACAAAGAC	TTTAACGAGG	AAGAAAAAGA	ATATTTTTTC	240
CTTACCTTAA	GCGATAAAAA	ACTCCCCAAA	CTCGCTTATG	ATGAGCTTTT	AAACTATCTT	300
TTTGA AAAAC	ATTTTACGA	TAACGATTTA	CACCTAAAGC	TAGATGCTAT	TTTCAATCGC	360
ATTTCTAGCA	ATAATGCCGA	GCTTTTAAAC	ACCAAAAGCA	CGGATGAAAC	CACTATCGCC	420
TTATTTGAAA	GCGTCTCACA	ATACATTAAT	GAAGGGCTCTA	AAAGGGCTAA	TTTACAAAGA	480
TCTTTATTAG	ACAAACTCAA	AAATTTTAAT	TTCAAACAAG	CTTTTTTTAA	TTTACAAAAC	540
CAACAAGGCT	ATGACTTTTT	CGCCCCCATT	TTTGAATACT	TACTCAAAGA	TTACAATAAT	600
AACAGCCGAG	GGACATACGC	CGAATACTAC	ACCCCTTTAA	GCATCGCTAG	CATCATTGCC	660
AAGCTTTTAG	TGAATAAACC	CACTCAAAGC	GTCAAATCT	ATGATCCAAG	CGCTGGCACA	720
GGAACGCTTT	TAATGGCATT	AGCCCCACAA	ATAGGCACCG	ATTCTTGAC	CCTTTATGCC	780
CAAGACATTT	CGCAAAAATC	CTTAAGAAATG	CTCAAACCTCA	ACCTGATTTT	AAACGACTTG	840
ACCCACTCTT	TAAGACACGC	CATTGAGGGA	AACACTTTGA	CTAACCCTTA	CCACTCCAAA	900
GACCACAAAG	GGAAAATGGA	TTTCATCGTG	AGTAACCCCC	CTTTCAAATT	GGATTTTTCC	960
AACGAGCATG	CCGAGATTTC	GCAAAACAAA	AACGATTTT	TCTTAGGCGT	GCCTAATATC	1020
CCTAAAAACG	ATAAAAGCAA	AATGCCCAT	TACACGCTCT	TTTTCCAGCA	TGCGCTGAAC	1080
ATGCTCAGTC	CAAAAGGTAA	GGGAGCTATA	ATCGTGCCAA	CCGGATTCT	TAGTGCTAAA	1140
AGCGGGGTAA	ATAATAAGAA	TGTCCGGCAT	TTAGTGGATG	AAAGGCTCGT	TTATGGGGTG	1200
ATTTGCATGC	CCAGTCAGGT	TTTGCCCAAC	ACCGGCACTA	ACGTGAGCAT	CATCTTTTTT	1260
CAAAAAACGC	CAAGCGCAAA	GGAAGTGATC	TTGATTGACG	CTTCCAAACT	CGGCGAAGAA	1320
TACACCGAAA	ACAAAAACAA	AAAAACGCGC	TTAAGACCAA	GCGATATGGA	TTTGATTTTA	1380
GAAACTTTCC	AAAATAAAGC	CCCAAATCG	GATTTTTCG	CTCTGGTTTC	TTTTGATGAA	1440
ATTACAGAAA	AAAATTATTC	TCTAAACCCC	GGGCAGTATT	TCATATAGA	AGACACGAGC	1500
GAGACAATCA	GCCAAGCGGA	GTTTGAAAAC	TTGATGCAAC	AATATTCAAG	CGAACTAGCG	1560
AGCCTTTTGTG	ATGAAAGCCA	AAATTTGCAA	CAAGAGATTT	TAGAACTTT	AAAAGGGGTT	1620
AGGTTTGAG						1629

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid

SUBSTITUTE SHEET (RULE 26)

861

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199

AAAGGGGATT TCATGAAAGA ACAAGATGCG GATTTAAGCG CTTTATTTGA AAATAAAGAA	60
AGCGCAGAAG AATTTTAA AACCCTTACAA ACAGAAGTGC AAGAATTTGA GAACGCTTAT	120
CAAAATAACC TTAAGAATTT AGACGCTGCA AAATTTGCCA ACACTCTTAA ACATTACGAA	180
AAATTTGTCAG AAAAGATCTC TAGAGCGATG GCTTACGCTC AATTACTTTT TGCCAAGAAC	240
ACTAAAGAAG CGAAGTTT TTCGCAATGC GAAATGGCTT GTGCAAATAT CCAACAACAC	300
CTTTTATTCT TTGAAATTGA ATTTAAGAAT TTGGACGCCA AAAAACAGCT CGCTTTCATT	360
AAAAAATGCA AAGATCATGC TTTTATTTA AACAATCTCA TAGAAAAGAA AAAGCACACC	420
CTAAATTTAG ATGAAGAAA GATCGCTCTA GCCCTTTCGC CTGTGGGAGT GGGTGCCTTT	480
AGCTTTGTTA TGGATGAACA TTTGTTTTCT TTGAACATCT CTTTACATAG AATAAACTTT	540
AAGCGAAGAA TAAATTTT CCCTCTTGCA CAACCC	576

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200

GCCAAAGAGC TTCTCAATGA GCCTGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA	60
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT	120
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTATAGAT	180
GTGGGGCGGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA	240
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC	300
CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT	360
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA	420
ATCGCCCTCG CTTCCCAACT TTTAGAAAT GATTTAAAG ACTCA	465

(2) INFORMATION FOR SEQ ID NO:1201:

SUBSTITUTE SHEET (RULE 26)

862

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201

ATGCCCTTTT	TAAAAGCCCT	AGCATCTTTT	GATGCGCCCT	TTTGTAGAAA	AGAAATTTC	60
AAGCGTTT	GGGATAATT	AGTTTTTTT	AAATCTTATC	ACCCTAATCT	GTTTAACGCC	120
CTCAATACGC	CTTTTAAAA	TTACCAATTG	CTTTTGTAAA	CAAACCATCT	TAATCTCTTA	180
CACACGCCCA	CGAACGCTT	AAGCTACCCT	AAACATCAAA	TGATAGAAAC	CGCTTTTAAC	240
ATGGCTAAAA	ACCCCTTGAA	TAATCCCAGA	TGGTCATTAG	ACAATAACCA	CCTCTCTTTA	300
CATTATTAA	AATCTCAAAA	CAACCACAAA	CTCCCCCTAA	CCCTTAAAGC	CACGCATGCG	360
ATCTCAAACT	TTTGTAGATA	TCATCAAACG	CCTTGCTCTT	TAAAGAAATT	CCTACCCCTT	420
ACCATGATT	ATGGCGTTT	AGACGGCTTG	TTTTTGGCTA	TTTTACAGGC	TCAAAATTAC	480
CGCTTCCATT	CGCTTTATTT	GTTTGAAGAA	AATTTAGACT	TGTTTAAAT	CAGTTGCTAT	540
TTTGCGCGTT	ATGAAGATT	GATTAAAAAA	GGGGCTAAAC	TTTTTATTCA	AGGGTTTTTT	600
AACCCTAATG	AATTGAAAAT	GGATTTTTTG	AAACGCCCTA	TCACGCATTG	TTTTTTAAAG	660
CTAGAAATCA	TGCCCTATAA	AAGCGCTTTT	AATTTGCGCA	TGCGAGAAAA	CATTCAAAGC	720
TATTACAAAC	AAGCCTTAAG	GGGTGGGGG	AGTTTGAAG	ACGAATTGCT	AGGGGTAAAG	780
AACACGCTTA	AAAACCTACC	CCTATGCCAA	ACCCTAAAAA	CCAAACCCAA	AAAAATTAAAC	840
GCCCCCATTT	GCGTGGTGGG	TAATGGGCCA	AGCCTGGATT	TATTGTTAGA	TTTTTTAAAA	900
GAAAATGAAG	AAAAATTTCAT	CATTTTTTCA	TGCGGAACCG	CTTTAAAGCC	TTTAAAAGCG	960
CATGGCGTTA	AAGTGGATT	TCAAATAGAA	GTGGAGCGCA	TAGACTATCT	TAAGGAGGTT	1020
TTAGAAAGAG	CCCCCCTAGA	AGACACCCCC	TTAATGGGCG	CTAACATGCT	CAATCCTAAC	1080
GCTTTTGATT	TAGCCAAAGA	AGCGTTGATG	TTTATGCGTG	GGGGGAGCGC	TTGCGCATAT	1140
AAGCCCTTGG	AGTATAGAA	ACGCAGCGCC	TTTTGTGGGC	AATGCCGGGG	TGGCTTTAGC	1200
GGGTTTGATG	AGCGA					1215

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1239

SUBSTITUTE SHEET (RULE 26)

863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202

AAGGGGTTAG	GTTTGAGTGA	GTGGCAAACA	TTTTGTTTAA	AAGATTTAGG	GAAAAATAGTC	60
GGCGGCGCTA	CCCCACCTAC	CAATAACCCC	AAAAATTATG	GCAATAAAAT	TGCTTGGATT	120
ACCCCTAAAG	ATTTATCCAC	TTTACAAGGG	CGCTACATTA	AAAAAGGCAG	CCGCAGCATT	180
TCACGATTAG	GGTTTAAATC	ATGCTCTTGT	GTGTTGCTCC	CAAAGCATGC	CATTTTATTT	240
TCTTCAAGAG	CTCCCATAGG	TTATGTGGCA	ATTGCTGAAA	AAAGGCTATG	CACCAATCAA	300
GGTTTTAAAA	GTATTATCCC	TAACAAAAAA	ATTTATTTTG	AATTTTATA	TTACTTATTA	360
AAATACTATA	AGGATAACAT	TTCCAACATA	GGGGGCGGAA	CTACTTTTAA	AGAAGTTTCA	420
GGGGCTACTT	TAGGTCTATT	CCAAGTTAAG	ATACCCCCCA	CTTATTACGA	ACAACAAAAA	480
ATCGCCCA	CACCTTCTAT	TTTAGATCAA	AAAATAGAGA	ACAACCATAA	AATCAATGAG	540
CTTTTACACA	AAATCTTAGA	GCTTCTTTAT	GAGCAATACT	TCGTCCGTTT	TGATTTTTTA	600
GATGAAAACA	ACAAACCCTA	TCAAACCTAGC	GGCGGAAAAA	TGAAATTTTC	TAAAGAATTA	660
AACCGCCTTA	TCCCTAACGA	TTTTAAAGTC	AAAACGCTAG	GGGAACATAA	AACTTGGATT	720
TCCGGAAGTC	AGCCACCCAA	AAGTTGTCAC	ATATACGAGT	ATAAAGAGGG	TTACATTCGT	780
TTCATACAAA	ACAGAGATTA	TAGCTCTAAT	AATTATGTTA	CATATATTCC	TATATCAAAA	840
AATAACAAGA	TTTGTTATCA	ATATGATATT	ATGATGGACA	AATACGGAGA	AGCTGGATCC	900
GTGCGTTTIG	GACTTCAAGG	GGCTTATAAT	GTTGCCTTAA	GTAAATTAG	CGTATTAAAT	960
CAATCCATGC	AGGAATATAT	ACGCAGTTAT	CTAAATTCAA	AACCTATAAA	AAAATATCTT	1020
TCTAATGCTT	GCATGGCATC	TACGAGAGCA	TCATAAATG	AAAATCATAT	TTATTCTTTA	1080
ATGCTCCCCA	TACCACCTAT	TAATCTATTA	CAAAAATACG	AAAAAATCGC	AAAAAATATC	1140
ATAACAGCCA	TTATTAAAAA	CAATCAATCA	ACCCAAACCC	TAACCGCGCT	CAGAGACTTT	1200
CTACTCCCCC	TACTCTTAAA	ACAACAAGTC	AAACCACAA			1239

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203

GGTGTAACCT	TAATTCAACA	AGAAGGATTT	ATTATGATTA	AAAGAATTGC	TTGTATTTTA	60
AGCTTGAGCG	CGAGTTTAGC	GTTAGCTGGC	GAAGTGAATG	GGTTTTTCAT	GGGTGCGGGT	120
TATCAACAAG	GTGCTTATGG	CCCTTATAAC	AGCAATTACT	CTGATTGGCG	TCATGGCAAT	180
GACCTTTATG	GTTTGAATTT	CAAATTAGGT	TTTGTAGGCT	TTGCCAATAA	ATGGTTTGGG	240
GCTAGGGTGT	ATGGCTTTTT	AGATTGGTTT	AACACTTCAG	GGACTGAACA	CACCAAAACC	300
AATTTGCTCA	CCTATGGCGG	CGGTGGCGAT	TTGATTGTCA	ATCTCATTCC	TTCGGATAAA	360
TTCGCTCTAG	GTCTCATTGG	TGGCGTTCAA	TTAGCCGGAA	ACACTTGGAT	GTTCCTTAT	420
GATGTCAATC	AAACCAGATT	CCAGTTCTTA	TGGAATTTAG	GCGGAAGAAT	GCGTGTGGG	480
GATCGCAGTG	CGTTTGAAGC	GGGCGTGA	TTCCCTATGG	TTAATCAGGG	TAGCAAAGAT	540
GTAGGGCTTA	TCCGCTACTA	TTCTTGGTAT	GTGGATTATG	TCTTCACTTT	C	591

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid

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864

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204

TTTCGCTTTT	ATTTCTTTAA	AGCAAATCGA	TCCTACTGGG	GAAAGGTTTT	TATGGTAAAC	60
AGCACACTTT	ATATTGTTAT	TGCCGGCTTA	TGGCTTGCTG	TAGGCTTTGG	AATCTTTTAA	120
AAGAAATTAG	ACATGCCCGT	TATCATTTGGC	TACATTTGCA	CAGGAACGGT	CTTAGCGGGT	180
TTTTTTAAAA	TTAATGATTT	TAATTTGTTG	TCTGATATTG	GTGAATTTGG	TATCGTCTTT	240
TTAATGTTTA	TGATAGGCAT	TGAGTTTAAT	TTTGACAAGC	TCAAGTCCAT	CAAACAAGAA	300
GTGCTCGTTT	TTGGGCTTTT	ACAGGTGTTT	TTATGCGCTT	TAATCGCTTT	TTTATTGGGG	360
TATTTGTGTC	TGGGTCTTTT	GCCCATTTTT	TCCCTTGTTT	TAGGCATGGG	GCTTTCACCTC	420
TCTTCAACCG	CCATTGTGTT	GAAATCTTTT	GAAGATTCCA	AACAGCTTAG	CACGCCTATG	480
GGAAAGAGCG	CGGTGGGGAT	TTTGATTTTC	CAAGATATTG	CAGCCATTCC	CATGCTTTTA	540
ATTTTGACGA	TTCTAGGCAG	TAAGGATTCT	CATGTCAATT	TGCTCATTCT	TAAAACCCTT	600
ATTTACGCCG	GGATTATTTT	AATTCTTTTA	TIATTGCCTG	AAAAAAAAGG	GGCTAATCTC	660
ATCTTAGAGC	AAGCGAAAGA	CACGCGCTTG	CCTGAAATCT	TTATAGGCAC	GGTTTTAGTG	720
ATTGTTTGCA	GCGCGGCGGG	GTTGAGCCAT	TTTTTTGGGT	TTCTATGTC	TTTGGGGGCG	780
TTCAATTGTG	GCATGGCGAT	TTCTAAATCG	CGCTATAAAA	TCAATGTCCA	AGAAGAATTC	840
GCGCAATTAA	AAAACCTCTT	TTTGCCCTTT	TTTTTCATTA	CGATAGGGAT	GCAGATTAAAT	900
GTGAGTTTCT	TCATGGAGAA	ATTCTTTGTC	GTCATCTTTT	TACTCAITTT	AGTGATGAGT	960
TTTAAGACTT	TTATCATTTA	TGCGCTATTG	CGTTTTTTTA	GAGACGCTAA	AACCGCCATC	1020
AAAACCGCTC	TTTCTTTTGG	GCAAATTGGG	GAGTTTTCTT	TCGTGATCTT	TTTAAATTCA	1080
GCGCTCGCAC	CAGCTCTT					1098

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205

TGTTTTATGCG	TGGGGGGAGC	GCTTGCGCAT	ATAAGCCCTT	TGAGTATAGA	ATACGCAGCG	60
CCTTTTGTGG	GCAATGCCCG	GGTGGCTTTA	GCGGGTTTGA	TGAGCGATGA	AATTTATTGG	120
TGCGCTTTAG	ATTGCGCTTA	TATCAAAGGG	TTTAAAAAGC	ACGCTCAAAA	TTCTATTAT	180

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